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(54) **DNA POLYMERASES**

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C12N 9/96 (2006.01)

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C12Q 1/68 (2006.01)

(52) **U.S. Cl.**

CPC **C12N 9/1252** (2013.01); **C12N 9/96**

(2013.01); **C12P 19/34** (2013.01); **C12Q**

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C12Q 1/6851 (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

Novel proteins having DNA polymerase are described which have utility in amplification reactions and have improved properties over Bst polymerase such as for example enhanced reverse transcriptase activity.

17 Claims, 5 Drawing Sheets

FIG. 1A
MELT PEAK

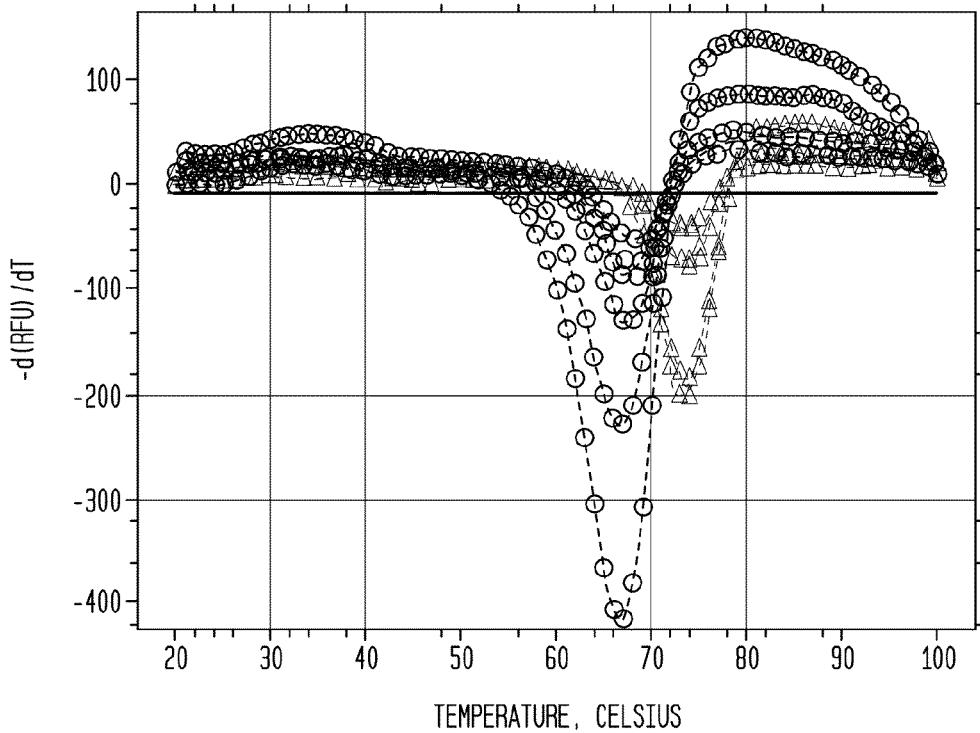


FIG. 1B

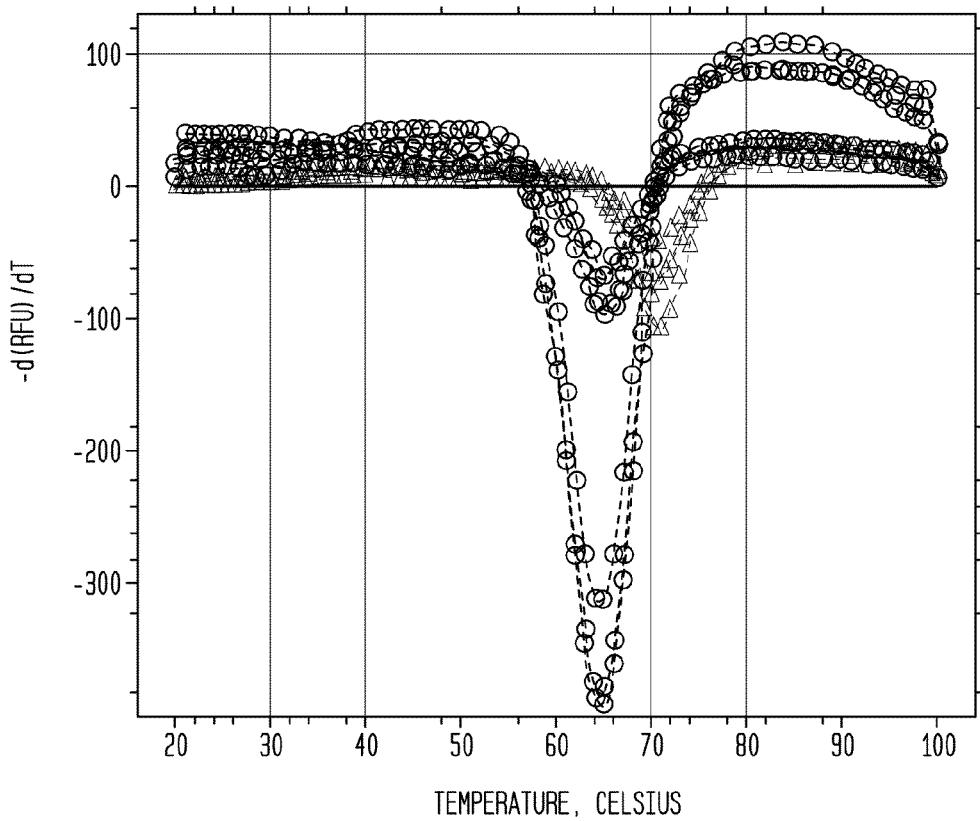


FIG. 2A
REACTION SPEED

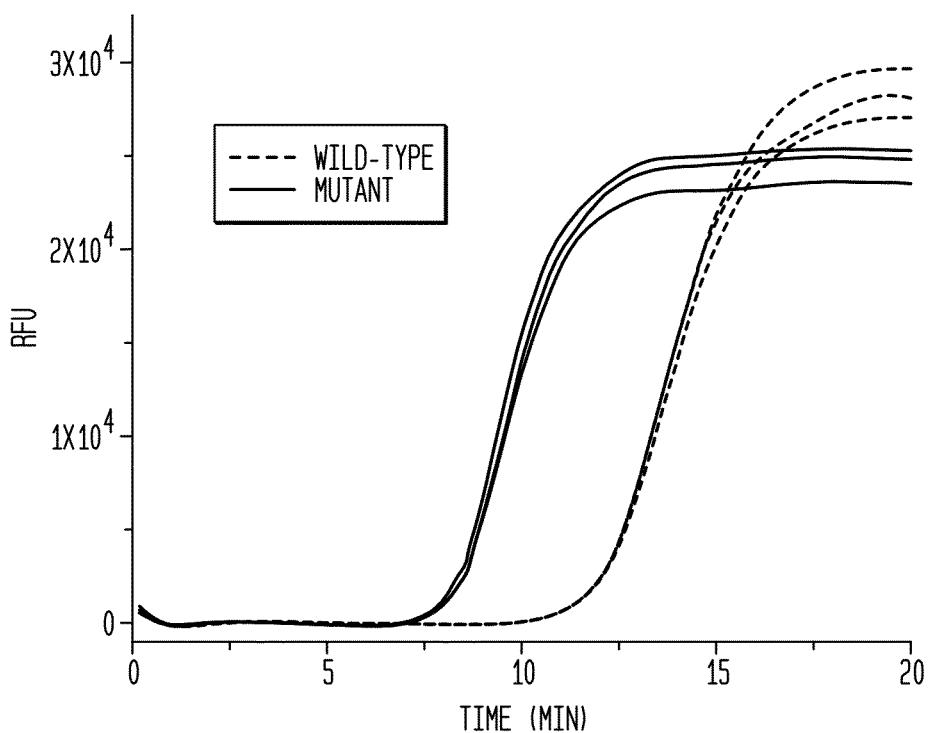


FIG. 2B
SALT TOLERANCE

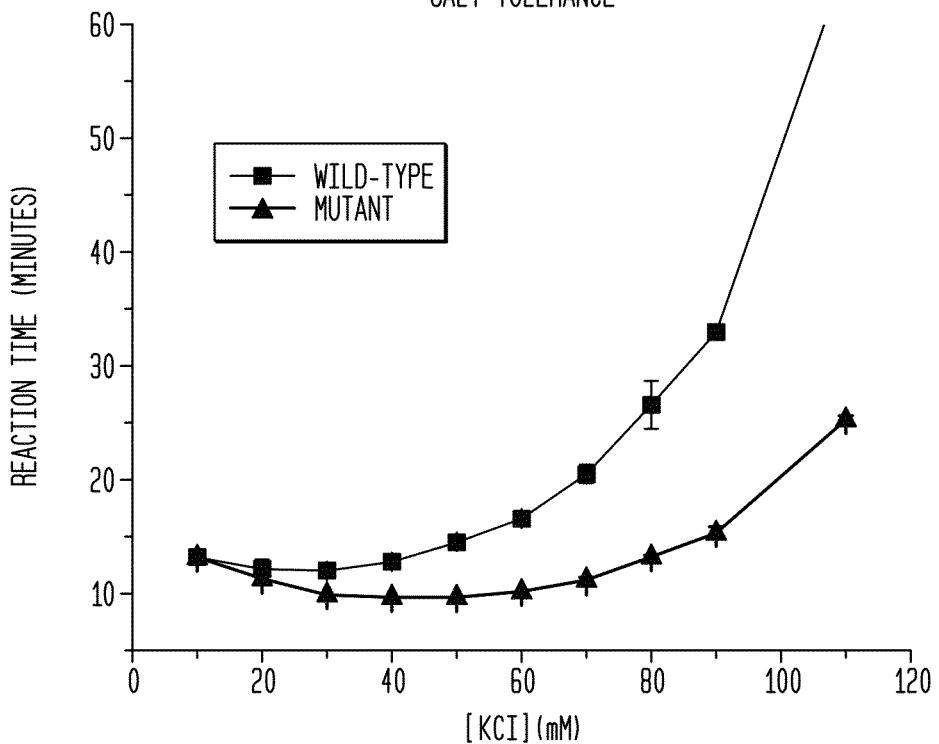


FIG. 2C

TEMPERATURE

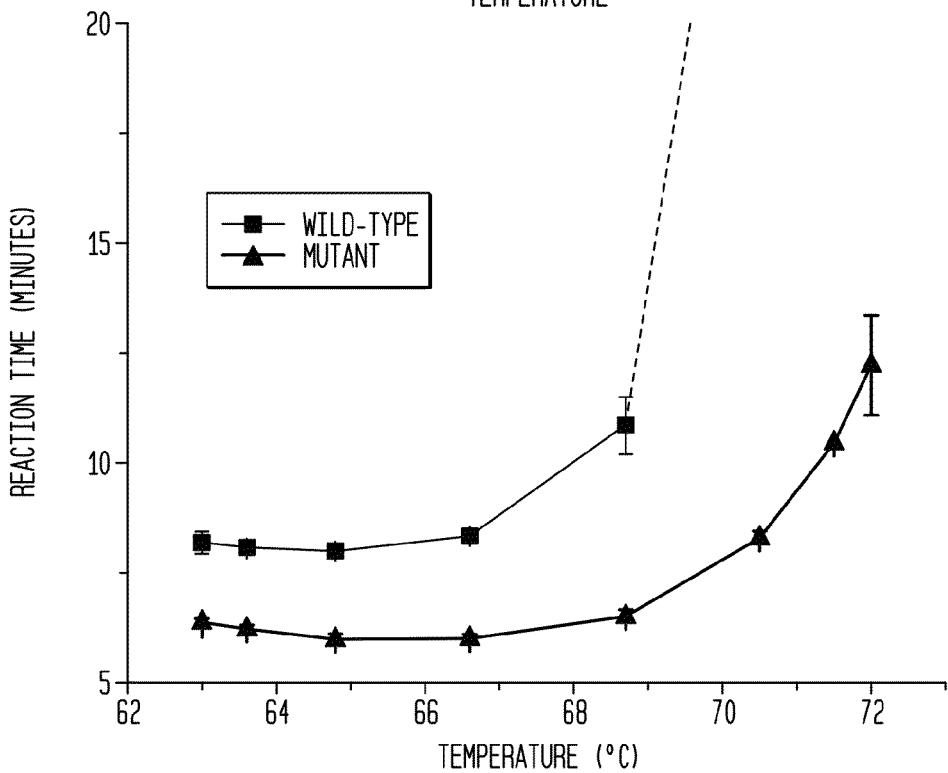


FIG. 2D

STORAGE STABILITY

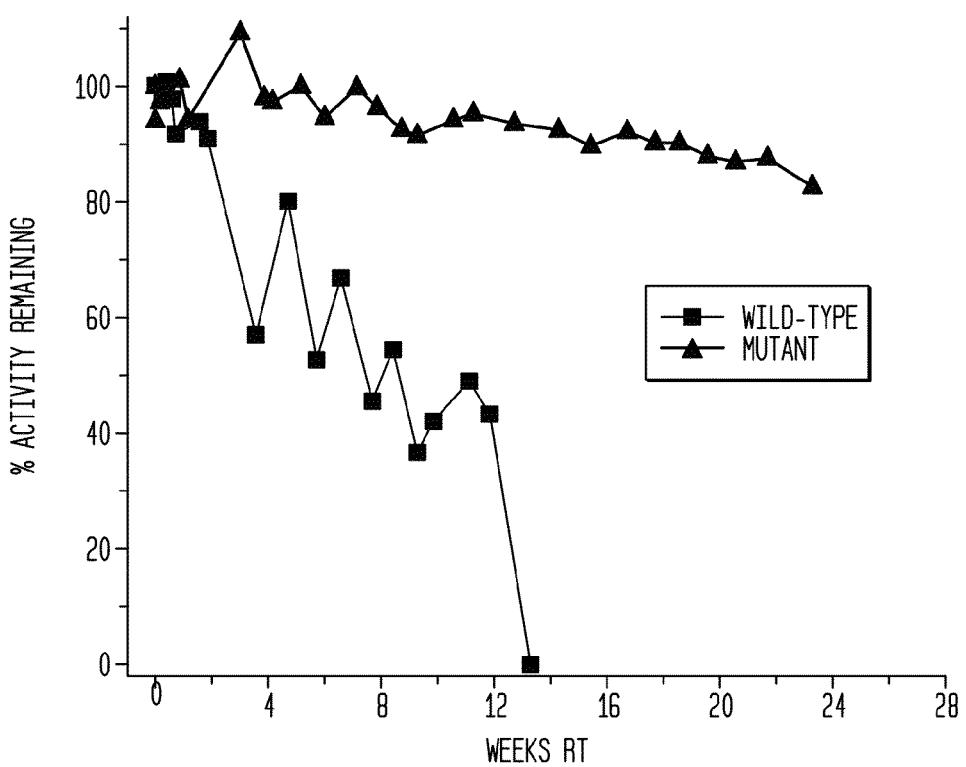


FIG. 2E
dUTP TOLERANCE

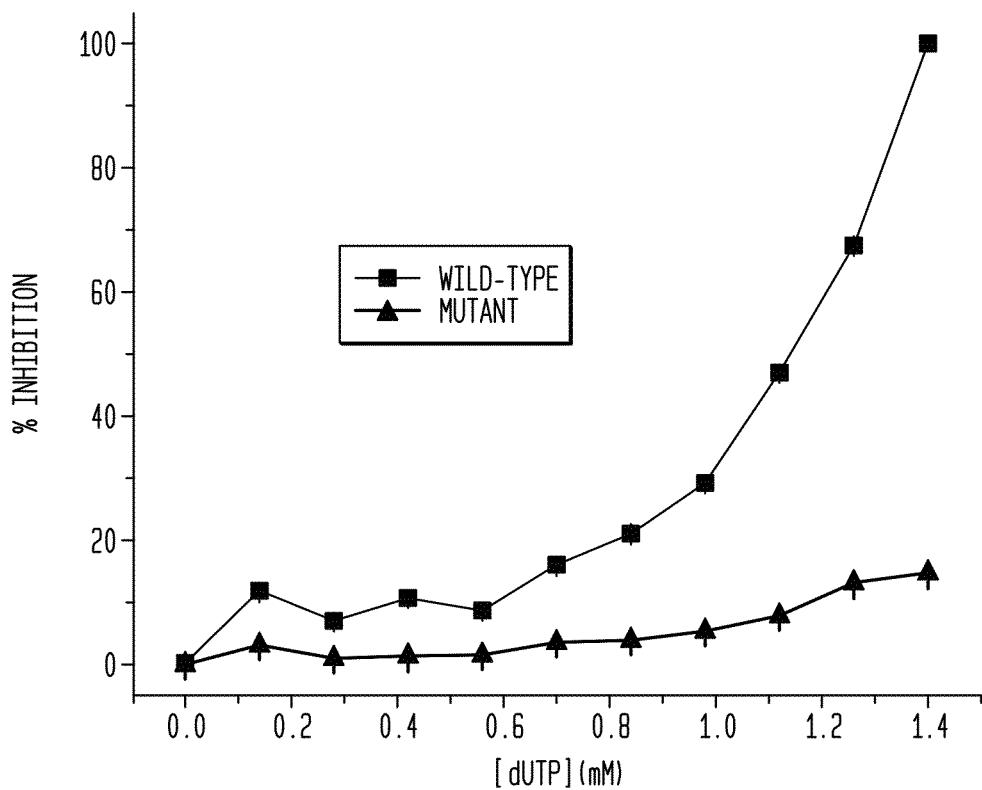


FIG. 3A

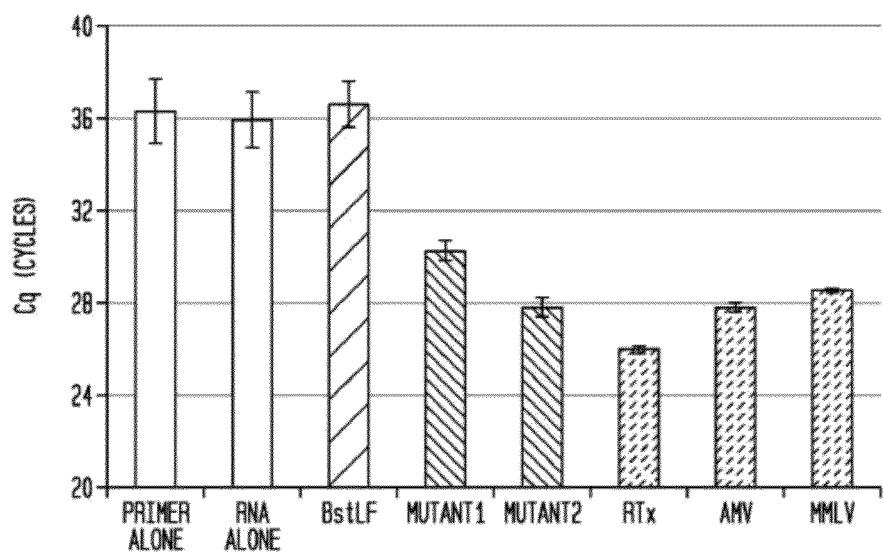
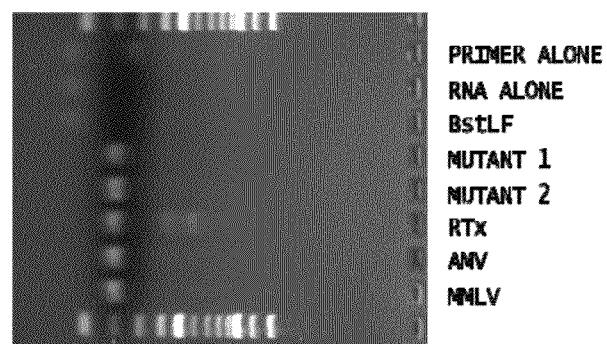


FIG. 3B



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DNA POLYMERASES

CROSS REFERENCE

This application is a continuation of U.S. Ser. No. 13/600, 408 filed Aug. 31, 2012, herein incorporated by reference.

BACKGROUND

A DNA polymerase from *Geobacillus stearothermophilus* has been described in Kong, et al., U.S. Pat. No. 5,814,506 (1998). This enzyme, which is a Bst DNA polymerase belongs to the Family A DNA polymerase and shares about 45% sequence identity with its better known relative Taq DNA polymerase. Whereas Taq DNA polymerase is from a hyperthermophilic organism and is able to survive the high temperatures of the polymerase chain reaction, the Bst DNA polymerase reported in Kong, et al., is from a thermophilic organism, is optimally active between 60-70° C., but does not survive the high temperatures of PCR. The full length (FL) Bst DNA polymerase is 876 amino acid residues and has 5'-3' endonuclease activity but not 3'-5' exonuclease activity. The large fragment (LF) of Bst DNA polymerase lacks both 5'-3' exonuclease activity and 3'-5' exonuclease activity and is only 587 amino acid residues with 289 amino acids being deleted from the N-terminal end. The full length Bst DNA polymerase and the large fragment Bst DNA polymerase have been found to be useful for isothermal amplification techniques and DNA sequencing.

SUMMARY OF EMBODIMENTS OF THE INVENTION

Compositions and methods are described herein that utilize novel improved synthetic DNA polymerases for isothermal DNA replication and other uses, the improvements being determined by comparison with a naturally occurring Bst polymerase.

In one embodiment, a protein consisting of a synthetic protein with polymerase properties is provided having at least 99% sequence identity with any of SEQ ID NOs:1-126.

In a second embodiment, a protein comprises an amino acid sequence that has at least 98% sequence identity with at least one sequence selected from SEQ ID NOs:1-42.

In a third embodiment, a protein comprises an amino acid sequence that has at least 99% sequence identity with at least one sequence selected from SEQ ID NOs:43-84.

In a fourth embodiment, a protein comprises an amino acid sequence that has greater than 98% sequence identity with at least one sequence selected from SEQ ID NOs:85-126.

In embodiment 5, a protein according to any of embodiments 1 through 4, further comprises DNA polymerase activity.

In embodiment 6, a protein according to any of embodiments 1 through 4 is capable of replicating DNA.

In embodiment 7, a protein according to embodiment 6, is capable of replicating DNA in an isothermal amplification reaction.

In embodiment 8, a protein according to any of embodiments 1 through 4 is contained in a storage buffer, or a reaction buffer.

In embodiment 9, a protein according to embodiment 8, is contained in a buffer that further comprises temperature dependent inhibitor of polymerase activity.

In embodiment 10, a protein according to any of embodiments 1 through 4 fused to a peptide either directly or by means of a linker.

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In embodiment 11, a protein according to any of embodiments 1 through 4, is contained in a buffer that further comprises dNTPs.

In embodiment 12, a DNA encodes the protein of any of the embodiments 1 through 4.

In embodiment 13, a host cell comprises the DNA according to embodiment 12.

In embodiment 14, a method for determining whether a protein according to any of embodiments 1 through 4 has improved polymerase activity compared with a wild type Bst polymerase; includes synthesizing a protein according to any of the embodiments 1 through 4; and determining polymerase activity.

In embodiment 15, a method according to embodiment 14 is described which includes characterizing the polymerase activity; and determining in comparison with a wild type Bst polymerase, at least one improved property selected from the group consisting of: thermostability; stability in storage; tolerance to salt; performance in isothermal amplification; strand displacement; kinetics; processivity; fidelity; altered ribonucleotide incorporation; 2'-deoxyuridine 5'-triphosphate incorporation; reverse transcriptase activity (Rtx) and modified nucleotide incorporation.

In embodiment 16, a method is described which includes:

(a) selecting a protein according to any of embodiments 1 through 4; and

(b) expressing the protein as a fusion protein with an additional peptide at an end of the amino acid sequence, the additional peptide attached either directly or by means of a linker.

In embodiment 17, a method of isothermal amplification is described that includes:

(a) providing a reaction mixture comprising a protein according to any of embodiments 1 through 4, primers and dNTPs;

(b) combining a target DNA with the preparation; and

(c) amplifying the target DNA at a temperature less than 90° C.

In embodiment 18, a method according to embodiment 17, is described where the amplification reaction results in a quantitative measure of the amount of target DNA in the preparation.

In embodiment 19, a protein according to any of embodiments 1 through 4 is further characterized by one or more improved properties for isothermal amplification compared with a wild type Bst polymerase, selected from the group consisting of:

(a) an increased reaction speed where the increase is at least 10% and as much as 200%, 500% or 1000%;

(b) an increased temperature stability in the range of 50° C.-100° C., 50° C.-90° C. or 60° C.-90° C.;

(c) an increased salt tolerance in the range of 10 mM-1 M, or 20 mM-200 or 500 mM monovalent salt;

(d) an increase in storage stability at 25° C., retaining at least 50% activity over 45 weeks, over 1 year, or over 2 years;

(e) an enhanced dUTP tolerance of the range of an increase of 50% to 100% dUTP; and

(f) an increased reverse transcriptase activity by at least 2 fold.

BRIEF DESCRIPTION OF THE FIGURES

FIGS. 1A and 1B show melt peaks for a Bst DNA polymerase FL or LF and synthetic DNA polymerases.

FIG. 1A shows the melt peaks for a synthetic DNA polymerase (FL) which has a melting temperature (T_m)=73.5° C. (Δ) and the parent Bst DNA polymerase (FL) has a T_m =68° C. (○).

FIG. 1B shows the melt peaks for a Bst DNA polymerase LF (○) which has a T_m =65° C. while the synthetic DNA polymerase (Δ) has a T_m =70° C.

The reactions were performed in 1× Detergent-free ThermoPol™ Buffer (New England Biolabs, Ipswich, Mass.) and 1× SYPRO® Orange (Life Technologies, Carlsbad, Calif.).

FIGS. 2A-E show how the properties of a synthetic DNA polymerase can be screened for significant beneficial properties using an isothermal amplification protocol (Notomi, et al., *Nucleic Acids Research*, 28:E63 (2000)) and lambda DNA.

FIG. 2A shows an analysis of reaction speed. The synthetic DNA polymerase shows faster DNA amplification than the parent Bst DNA polymerase.

FIG. 2B shows the results of an assay to determine salt tolerance. The time in which the amplification reaction took to reach a threshold level of product was graphed against increasing KCl concentration in the reaction. The synthetic DNA polymerase was more tolerant to changes in salt concentration than the parent Bst DNA polymerase.

FIG. 2C shows the results of an assay to determine an increase in thermostability of a synthetic DNA polymerase by at least 3° C. compared with the Bst DNA polymerase. The time in which the amplification reaction took to reach a threshold level of product was graphed against increasing reaction temperature. The synthetic DNA polymerase was able to amplify DNA at a higher temperature than the naturally occurring Bst DNA polymerase.

FIG. 2D shows the results of an assay for storage stability in which a synthetic DNA polymerase remains stable for at least 28 weeks at room temperature (22° C.) versus about 13 weeks for the Bst DNA polymerase (8000 U/ml for each enzyme was used).

FIG. 2E shows the results of an assay for dUTP tolerance in which a Bst DNA polymerase is significantly inhibited by increasing amounts of dUTP while the synthetic DNA polymerase activity is relatively stable as dUTP levels increase (1.4 mM dUTP corresponds to complete substitution of dTTP with dUTP). The ability to incorporate dUTP without inhibition of the polymerase is a useful feature of a DNA polymerase for various applications including strand modification and differentiation. Thermophilic archaeal DNA polymerases do not amplify DNA effectively in the presence of dUTP. Taq DNA polymerase can incorporate dUTP into substrate but Taq DNA polymerase is not suitable for isothermal amplification because it is not capable of the requisite amount of strand displacement.

3A and 3B shows that the DNA polymerase mutants described herein with improved polymerase activity also have improved reverse transcriptase activity.

FIG. 3A shows the results of determining Rtx activity using RT-qPCR. The lower the value of cycles (C_q) the greater the activity of the Rtx. From left to right, the bar chart shows Primer alone, RNA alone, Bst polymerase large fragment (BstLF), 2 mutants of the DNA polymerase described herein, Rtx, Avian Myeloblastosis Virus Reverse Transcriptase (AMV) and Moloney Murine Leukemia Virus Reverse Transcriptase (MMLV).

FIG. 3B shows gel electrophoresis of amplified DNA resulting from an RNA template and BstLF DNA polymerase or mutants.

The lanes are labeled left to right as follows: Primer alone, RNA alone, BstLF, Mutant 1 and 2, Rtx, AMV and MMLV.

DETAILED DESCRIPTION OF THE EMBODIMENTS

As used herein, the term “synthetic” with respect to proteins or peptides refers to a non-naturally occurring amino acid sequence that is generated either by expression of a gene encoding the non-naturally occurring amino acid sequence or is generated by chemical synthesis. The gene encoding the non-naturally occurring amino acid sequence may be generated, for example, by mutagenesis of a naturally occurring gene sequence or by total chemical synthesis.

A “variant” or “mutant” protein refers to a protein that differs from a parent protein by at least one amino acid that is the product of a mutation. A variant polymerase is intended to include a “synthetic” protein and vice versa as the context permits. The examples utilize a variant DNA polymerase but it will be understood to a person of ordinary skill in the art that the assays described in the examples are applicable to analyzing synthetic proteins also.

“Non-naturally occurring” refers to a sequence or protein that at the date in which the embodiments of the invention are presented herein, no naturally occurring amino acid sequence corresponding to the alleged non-naturally occurring amino acid has been described in the publically available databases.

“Isothermal amplification” refers to a DNA amplification protocol that is conducted at a temperature below 90° C. after an initial denaturation step, where an initial denaturation step is required.

98% percent sequence identity may be calculated by any method known in the art such as for example, using the BLOSUM62 matrix and the methods described in Henikoff, et al., *PNAS*, 89 (22):10915-10919 (1992).

We have developed a set of proteins that have properties of the type observed for DNA polymerases belonging to Family A DNA polymerases. These proteins have improved polymerase activity when compared with wild type Bst DNA polymerase.

The DNA polymerase may have one or more improved properties as compared with the wild type Family A DNA polymerases such as those including one of specific activity, reaction speed, thermostability, storage stability, dUTP tolerance, salt tolerance and reverse transcriptase activity.

The proteins described herein generally retain DNA binding properties making these synthetic proteins useful for example as DNA detection reagents. The variants may be screened using at least one method described in Examples 1-6, or by other screening methods common used in the art, so as to identify those variants having at least one of the functional properties that are at least typical of a Family A DNA polymerase and/or have one or more improved properties selected from at least one of specific activity, reaction speed, thermostability, storage stability, dUTP tolerance and salt tolerance, increased performance in isothermal amplification, non-interference of pH during sequencing, improved strand displacement, altered processivity, altered ribonucleotide incorporation, altered modified nucleotide incorporation, reverse transcriptase activity, and altered fidelity when compared to the corresponding parent polymerase. The improved properties of these mutant enzymes have been demonstrated to enhance the performance of sequencing platforms (for example, the Ion Torrent™ sequencer (Life Technologies, Carlsbad, Calif.)). The improved properties of these mutant enzymes enhance their use in isothermal amplification for diagnostic applications.

The DNA polymerase variants and synthetic proteins described herein may be expressed in suitable non-native host cells such as *E. coli* according to standard methods known in the art. To facilitate expression, the variant DNA polymerase may additionally have a methionine in front of the first amino acid at the N-terminal end. Host cells may be transformed

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with DNA encoding the variant optionally contained in a suitable expression vector (see New England Biolabs catalog 2009-10 or 2011-12 for expression vectors known in the art for this purpose). Transformation is achieved using methods well known in the art.

The DNA polymerase variants and synthetic proteins characterized herein may further be modified by additions and/or deletions of peptides at their N-terminal and/or C-terminal ends. For example, fusion of a peptide to a synthetic protein may include fusion of one or more of a DNA binding domain (such as Sso7d from archaea), an exonuclease domain (such as amino acids 1-289 of Bst DNA polymerase), a peptide lacking exonuclease activity (for example a mutated exonuclease domain similar to amino acids 1-289 of Bst DNA polymerase), an affinity binding domain such as a Histidine tag, chitin binding domain, or intein, and a solubility tag such as maltose binding domain or an antibody. The addition of a peptide fused to an end of the amino acid sequence of the DNA polymerase may be used to enhance one or more of the functional features described in Examples 1-6. Aptamers may be added to the preparation of the mutant DNA polymerase to enhance temperature sensitive amplification.

The proteins described herein may be stored in a storage or reaction buffer that includes a detergent such as a non-ionic detergent, a zwitterionic detergent, an anionic detergent or a cationic detergent. The storage or reaction buffer may further include one or more of: a polynucleotide, for example, an aptamer for facilitating a hot start; polynucleotide primers, dNTPs, target polynucleotides; additional polymerases including additional DNA polymerases; RNA polymerases and/or reverse transcriptases; crowding agents such as polyethylene glycol; and/or other molecules known in the art for enhancing the activity of the DNA polymerase variants.

The DNA polymerase variant and synthetic proteins may be used for DNA synthesis, DNA repair, cloning and sequencing (see for example U.S. Pat. No. 7,700,283 and US Application Publication No. US 2011/0201056) and such as illustrated in the examples and also for temperature dependent amplification methods. Examples of isothermal amplification methods in addition to loop-mediated isothermal amplification (LAMP) used in the present examples include helicase dependent amplification (HDA) (see for example U.S. Pat. No. 7,829,284, U.S. Pat. No. 7,662,594, and U.S. Pat. No. 7,282,328); strand displacement amplification (SDA); nicking enzyme amplification reaction, recombinase polymerase amplification, padlock amplification, rolling circle amplification, and multiple displacement amplification (see for example Gill, et al., *Nucleosides, Nucleotides and Nucleic Acids*, 27:224-243 (2008)). The proteins described herein may also be used in sample preparation for sequencing by synthesis techniques known in the art. The proteins may also be used in quantitative amplification techniques known in the art that may be performed at a temperature at which the variant or synthetic protein effectively polymerizes nucleotides.

EXAMPLES

The Examples provided below illustrate assays for the Bst DNA polymerase variants described herein.

Example 1

Assay for Determining the Properties of a Variant DNA Polymerase

(a) Loop-mediated isothermal amplification (LAMP)

The properties of a variant polymerase can be determined using an isothermal amplification procedure such as a LAMP

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protocol (Nagamine, et al., *Mol. Cell. Probes*, 16:223-229 (2002); Notomi, et al., *Nucleic Acids Research*, 28:E63 (2000)).

The LAMP reaction used bacteriophage X genomic DNA (New England Biolabs, Ipswich, Mass.) as the template. The LAMP primers used here were:

FIP

(SEQ ID NO: 127)

(5' -CAGCCAGCGCAGCACGTTCGCTCATAGGAGATATG
GTAGAGCCGC-3') ,

BIP

(SEQ ID NO: 128)

(5' GAGAGAAATTGTACCACCTCCCACGGGCACATAGC
AGTCCTAGGGACAGT-3') ,

F3

(SEQ ID NO: 129)

(5' -GGCTTGGCTCTGCTAACACGTT-3') ,

B3

(SEQ ID NO: 130)

(5' -GGACGTTGTAAATGTCGGCTCC-3') ,

LoopF

(SEQ ID NO: 131)

(5' -CTGCATACGACGTGTCT-3') ,

LoopB

(SEQ ID NO: 132)

(5' -ACCATCTATGACTGTACGCC-3') .

The LAMP reaction used 0.4 U-0.2 U variant Polymerase/ μ L, 1.6 μ P/BIP, 0.2 μ M F3/B3, 0.4 μ M LoopF/LoopB, and 5 ng λ DNA in a buffer containing 1x Detergent-free ThermoPol, 0.1% Tween 20, 6-8 mM MgSO₄ and 1.4 μ MdNTP. The reaction was followed by monitoring turbidity in real time using the Loopamp® Realtime Turbidimeter LA-320c (SA Scientific, San Antonio, Tex.) or with a CFX96™ Real-Time fluorimeter (Bio-Rad, Hercules, Calif.). The reaction conditions were varied to determine the optimum range that the variant DNA polymerase could perform LAMP. This was compared with the parent Bst DNA polymerase. The parent Bst DNA polymerase was typically used at 65° C. in these LAMP reaction conditions. However, the temperature was varied to determine the optimum temperature for a particular variant. Different salt conditions and rates of reaction were tested and variants identified which were 10%-50% faster than the parent polymerase and had an increased salt tolerance to as much as 200 mM KCl. The results are shown in FIG. 2.

(b) DNA polymerase activity assay using modified nucleotides in a comparison of the activity of a fusion variant protein with exonuclease activity, with full length parent Bst polymerase

This assay was used to determine the activity of the variant polymerase having exonuclease activity as a result of an additional 289 amino acid sequence at the N-terminal end that has been described in detail for parent DNA Bst polymerase. The activity was measured by incorporation of a radioactive ³H-dTTP in a DNA substrate using various concentrations of a variant polymerase. A DNA polymerase reaction cocktail (40 μ L) was prepared by mixing 30 nM single-stranded M13mp18, 82 nM primer #1224 (5'-CGCCAGGGTTTC-CCAGTCACGAC-3') (SEQ ID NO:133), 200 μ M dATP, 200 μ M dCTP, 200 μ M dGTP, and 100 or 200 μ M dTTP including 0.6 to 0.8 μ Ci [3H]-dTTP. The DNA polymerase reaction cocktail was mixed with DNA polymerase (2.2 to 8.7 ng for the parent Bst DNA polymerase (FL), 0.27 to 1 ng for the fusion variant, or 2.5 to 20 ng for the parent Bst DNA poly-

merase LF), or water for the no enzyme control, and incubated at 65° C. for 5 minutes. Reactions were halted and precipitated by acid precipitation as follows. A 30 μ l aliquot of each reaction was spotted onto 3 mm Whatman discs and immediately submerged into cold 10% Trichloroacetic acid (TCA) in 1 L beaker in an ice bucket. A total counts control was spotted as described but not washed. Filters were washed three times with cold 10% TCA for 10 minutes with vigorous shaking and twice with room temperature 95% isopropanol for 5 minutes. Filters were dried under a heat lamp for 10 minutes and counted using a scintillation counter. The pmoles of dNTPs incorporated were calculated for each sample from the fraction of radioactive counts incorporated, multiplied by the total amount of dNTPs and the volume of the reaction.

A tenfold increase in specific activity of the fusion variant polymerase was found compared with the parent FL Bst polymerase where the fusion variant DNA polymerase was present in the mixture at 506,000 U/mg while the parent Bst DNA polymerase was present at 48,000 U/mg (1 unit=incorporation of 10 nmol dNTP in 30 minutes at 65° C.).

A 15% increase in activity of the variant polymerase compared with the parent BstLF DNA polymerases was observed in which the variant DNA polymerase was present in the mixture at 370,000 U/mg and the parent DNA polymerase Bst (LF) was present at 260,000 U/mg.

Example 2

Variant DNA Polymerase Thermostability

The thermostability of the variant DNA polymerase was assessed by incubating the polymerase at differing temperatures followed by performing either one or both of the DNA polymerase assay described in Example 1. The results are shown in FIG. 2C.

Example 3

Inhibitor Resistance of the Variant DNA Polymerase

The resistance of a variant DNA polymerase to inhibitors such as blood is determined by adding increasing concentrations of the inhibitor into the DNA polymerase assay and determining the change, if any, in the apparent specific activity of the protein. The DNA polymerase assay was performed as described in Example 1 at 65° C.

Another inhibitor of DNA polymerase is dUTP which is used to prevent carryover contamination in isothermal amplification by replacing dTTP. In this case it is desirable for the polymerase to be insensitive to dUTP inhibition so as to utilize dUTP as a substrate for LAMP. FIG. 2E shows that the mutant polymerase can efficiently utilize dUTP while the wild type Bst polymerase is inhibited by substituting dTTP with dUTP in the amplification reaction.

Example 4

Increased Resistance to High Salt Concentration

The resistance of a variant DNA polymerase to increased salt concentration was determined by adding increasing concentrations of salt (for example, KCl or NaCl) to the DNA polymerase assay described in Example 1 and determining the activity of the protein at 65° C. and comparing its activity to parent Bst DNA polymerase (see FIG. 2B).

Example 5

Increased Stability in Storage

The stability of a variant DNA polymerase during storage was determined by incubating the enzyme in storage buffer (10 mMTris-HCl pH 7.5, 50 mM KCl, 1 mM Dithiothreitol, 0.1 mM EDTA, 50% Glycerol, 0.1% Triton X-100) at a temperature ranging from 4° C. to 65° C. for a time period ranging from 1 day to 28 weeks, and assaying DNA polymerase activity remaining after storage using the LAMP method described in Example 1. The remaining activity was compared to a sample stored at -20° C. for the same amount of time. The stability of the variant was then compared to the stability of parent Bst DNA polymerase (See FIG. 2D). When this period was extended to 60 weeks, no detectable loss of activity of the mutants was observed even in the absence of glycerol.

Example 6

Assay for Determining the Melting Temperature of a Variant Polymerase for Comparison with a Parent DNA Polymerase using a SYPRO Orange Assay

The assay was performed as follows: Each 50 μ l reaction contains 1 \times Detergent-free ThermoPol Buffer (20 mM Tris-HCl pH 8.8, 10 mM $(\text{NH}_4)_2\text{SO}_4$, 10 mM KCl, 2 mM MgSO₄, 1 \times SYPRO Orange protein gel stain, and DNA polymerase concentrations ranging from 2.2 to 17.5 μ g (parent BstLF mutant) or 0.6 to 4.8 μ g (parent Bst FL mutant). The reactions were placed in a CFX96 Real-Time System. The temperature was raised 1° C. per second from 20° C. to 100° C., and the fluorescence (in the FRET channel) was read at each temperature. Here, the melting temperature (T_m) is the inflection point of the sigmoidal curve of fluorescence plotted against temperature. The inverted first derivative of the fluorescence emission in FIGS. 1A and 1B is shown in relation to temperature, where the location of the minima corresponded to the value of the melting temperature (see FIG. 1).

Example 7

Whole Genome Amplification using a Variant Bst DNA Polymerase

The variant DNA polymerase can be tested for suitability in whole genome amplification using the methods termed hyperbranched strand displacement amplification (Lage, et al., *Genome Research*, 13 (2):294-307 (2003)) or multiple-strand displacement amplification (Aviel-Ronen, et al., *BMC Genomics*, 7:312 (2006)).

Example 8

DNA Sequencing on a Semiconductor Device using a Variant DNA Polymerase

The variant DNA polymerase can be tested for its suitability in DNA sequencing, for example, as described in Rothberg, et al., *Nature*, 475(7356):348-352(2011)), an integrated semiconductor device enabling non-optical genome sequencing.

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Example 9

Solid-phase DNA Amplification using a Variant Polymerase

Variant DNA polymerase can be tested for its suitability in solid-phase DNA amplification, for example as described in (Adessi, et al., *Nucleic Acids Research*, 28:E87 (2000)), which describes a method for the amplification of target sequences with surface bound oligonucleotides.

Example 10

Enhanced Reverse Transcriptase Activity

The reverse activity of the mutant Bst DNA polymerase was determined using a two-step RT-qPCR assay. The first step was for complementary DNA (cDNA) synthesis using the mutant enzymes and various traditional reverse transcriptases. The second measures the amount of synthesized cDNA by qPCR. The RT step was performed using 6 uM Hexamer (Random Primer Mix, New England Biolabs, Ipswich, Mass.) as primers in Isothermal Amplification Buffer (New England Biolabs, Ipswich, Mass.) supplemented with 6 mM Mg and 200 uM dNTP with 0.1 ug Jurkat Total RNA (Life Technologies, Carlsbad, Calif.) and incubated at 65° C. for 20 minutes. 1 uL of the RT product was added to qPCR reaction for GAPDH gene with 200 nM of forward

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(5'AGAACGGGAAGCTTGTCACT) (SEQ ID NO:134) and reverse primer (5'CGAACATGGGGCATCAG) (SEQ ID NO:135), 200 uM dNTP, 1.25 unit of Taq DNA polymerase in 25 uL of 1x Standard Taq Buffer (New England Biolabs, Ipswich, Mass.) containing 2 uM of dsDNA-binding fluorescent dye SYTO®9 (Life Technologies, Carlsbad, Calif.). The PCR cycles were: 95° C. for 1 minute, then 50 cycles at 95° C. for 10 seconds, 61° C. for 15 seconds and 68° C. for 30 seconds, and a final step of 68° C. for 5 minutes. The PCR 10 was performed on a CFX96 Real-Time PCR machine and the Cq value was obtained as an indication of the amount of specific cDNA being synthesized (FIG. 3A). Mutant 1 and mutant 2 (4th and 5th bar from left in bar chart) make abundant cDNA as indicated by having Cq values similar to that of 15 traditional RTs (6th, 7th and 8th bar from left) in qPCR. Wild type BstLF (3rd bar from the left) is the same as controls (1st and 2nd bar from left) without RT. After completion of the 20 PCR reaction, 10 uL of PCR product was analyzed by electrophoresis in a 1.5% agarose gel (FIG. 3B) to verify the size 25 of the PCR product. The lanes from left to right are primer alone, RNA alone, BstLF, mutant 1, mutant 2, Rtx, AMV and MMLV. Mutant 1, mutant 2 and all RTs (Rtx, AMV and MMLV) lanes gave a band of expected size (207 base pairs) but no specific band with wild type BstLF or controls. These results demonstrate that mutant 1 and mutant 2 has much improved Rtx activity compared to wild type BstLF.

All references cited herein are incorporated by reference. Sequences

SEQ ID NO: 1
 EEEEKPLEDIEFAIADEITEEMLADKAALVVEVMEENYHDAPIVGIANVNNEHGRFFLRPETALASPQF
 KAWLADETKKKSMPDAKRAIVALWKGIELRGVAFDLAAAYLLNPAQTAEDIAAVAKMKQYEAVRSD
 EAVYGKGVKRSLSLPDEQALAEHLVRKAAAIIWALEQPFMDDLRLRKNEQDRLLTEEQPLASI LAEMEFTGV
 NVDTKRLEQMGSELAEQLKEQEQRIFYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTGRLSSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLIAHIADDNLIEAFQRDLIDIHTKTAMDIFHVSEEEV
 TANMRQQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASFPGVKEYMENIVQEAQKQGYVTT
 LLHRRRYLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAMIDLARLKEEQLQARLLLQVHDELI
 LEAPKEEIERLCKLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 2
 AEEEKPLEEMEFTDVDEITEEMLADKAALVVEVQEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 VAWLEDETKKKSMPDAKRAIVALWKGIELRGVAFDLAAAYLLNPAQDDDDVAAVAKMKQYEAVRSD
 EAVYGKGAKRSLSLPDEPTLAEHLVRKAAAIRALEQPFIDELRRREQDELFTKLEQPLATI LAEMEFTGV
 KVDTKRLEQMGSELAEQLKEVEQRIFYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTGRLSSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLIAHIADDNLIEAFRRDLIDIHTKTAMDIFHVSEEEV
 TANMRQQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASFPGVKEYMENIVQEAQKQGYVTT
 LLHRRRYLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAMIDLARLKEEQLQARLLLQVHDELI
 LEAPKEEIERLEQLPEVMEQAVRLRVPLKVDYHYGPTWYDAK

SEQ ID NO: 3
 EEEEKPLAEMEFTIADEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNERGRFFLRTETALADPQF
 KAWLADETKKKSMPDAKRAIVALWKGIELRGVDFDLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYGKGAKRALPDEPTLAEHLVRKAAAIIWALEEPFLDELRENEQDELLTEEQPLALILAEMEFTGV

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KVDTKRLEQMGEELAQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHREIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTGRLLSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFQSFPGVKRYMEDIVQEAKQKGYVTT
 LLHRRRYLPDITSRNPNVRSFAERTAMNTPIQGSAADI IKKAMIDLAARLKEERLQARLLLQVHDELI
 LEAPKEEIERLCKLVPEVMEQAVELRVPLKVDYRYGPTWYDAK

SEQ ID NO: 4

AEEEKPLEDIEFDIADEVTEEMLAADKAALVVEVQEDNYHDAPIVGFAIVNEHGRFFIRTELASQF
 KAWLADETKKSVFDAKRAIVALWKGIELRGVDFDLLLAAAYLLNPAQTADDVAAVAKMKQYHAVRSD
 EAVYGKGAKRAVPDEPVLAELVRKAAAIWALEEPFLDELRKNEQDELLTELEPLALILAEMEFTGV
 KVDTKRLEQMGEELAQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTGRLLSSTDPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNLIEAFRRDLDIHTKTAMDVFHVSEDEV
 TSNMRRQAKAVNFGIVYGISDYGLSQNLGIITRKEAAEFIERYFESFPGVKEYMEDIVQEAKQKGYVTT
 LLHRRRYLPDITSRNPNVRSFAERTAMNTPIQGSAADI IKKAMIDMAARLKEERLQARLLLQVHDELI
 FEAPKEEIERLCKLVPEVMEHAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 5

TEEEVELEDINVKTVTETVSEMLTDPSALVVEQLGDNYHEADIIGFAIVNENGAFFIPKETALQSEAF
 KEWVEDETKKKWFDSKRAVVALRHGIELKGVDVDLLASYIINPSNSYDDVASVAKERGLNIVSSD
 EAVYGKGAKRAVPAEDELAEHGRKAAIASALRDKLQLQALEENDQYELFEDLEPLALILGEMESTGV
 KVDVERLKRMGEELTEKLKEYEKEIHELAGEPFNINSPKQLGVILFEKLGLPVIKKTKGYSTSADVL
 EKLADKHIEIIRYILHYRQIGKLQSTYIEGLLKVTRKDTHKVHTRFNQALTQTGRLLSSTDPNLQNIPIR
 LEEGRKIRQAFVPSEEGWLIFAADYSQIELRVLAHISKDENLIEAFTHDMDIHTKTAMDVFHVSEDEV
 TSAMRRQAKAVNFGIVYGISDYGLSQNLGIITRKEAGAFIERYLESFPGVKAYMEDIVQEAKQKGYVTT
 LLHRRRYIPEITSRNPNVRSFAERTAMNTPIQGSAADI IKKAMIDMAARLKEENLQARLLLQVHDELI
 FEAPKEEIEILEKIVPEVMEHALELDVPLKVDYASGPSWYDAK

SEQ ID NO: 6

EEEEVPLEEIEFAIADEVTEEMLAADKAALVVEVLEENYHDAPIVGFALVNEHGRFFIRPETALASSQF
 KAWLEDETKKSVFDAKRAIVALWKGIELRGVDFDLLLAAAYLLNPAQSAEDVAAVAKMKQYEAURSD
 EAVYGKGAKRAVPDEPVLAELVRKAAAIWALEEPFLDELRENEQDELFLEQPLALILAEMEFTGV
 KVDTKRLEQMGEELAQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTGRLLSSTEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLSQNLNIITRKEAAEFIERYFASFPGVKQYMEMIVQEAKQKGYVTT
 LLHRRRYLPDITSRNPNVRSFAERTAMNIPIQGSAADI IKKAMIDLAARLKEERLQARLLLQVHDELI
 LEAPKEEIERLCKLVPEVMENAVTLRVPLKVDYHYGPTWYDAK

SEQ ID NO: 7

AEEEAPLEDIEFDIADEVTEEMLAADKAALVVEVQEDNYHDAPIVGFAIVNERGRFFIRTELASEAF
 KAWLADETKKSVFDAKRAIVALWKGIELRGVDFDLLLAAAYLLNPAQTADDVAAVAKMKQYHAVRSD
 EAVYGKGAKRAVPDEPVLAELVRKAAAIWALEEPFLDELRKNEQDELFTELEPLALILAEMEFTGV
 KVDTKRLEQMGEELAQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHREIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTGRLLSSTDPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNLIEAFRRDMDIHTKTAMDVFHVSEDEV

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TSNMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAAEFIERYFQSFPGVKEYMEDIVQEAKQKGYVTT
 LLHRRRLPEITSRNFNLRSPAERTAMNTPIQGSAADIICKAMIDMAARLKEERLQARLLLQVHDELI
 FEAPKEEIERLEKLVPVMEHAVELRVPLKVDYRYGPTWYDAK

SEQ ID NO: 8
 AEEEKPLEEMEFAIADEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 KAWLADETKKSMFDKRAIVALWKGIELRGVAFDLLAAYLLNPAQDADDVAAVAKMKQYEAVRSD
 EAVYKGAKRAVPDEPVLAELVRAAAIRALERPFLDELRNNEQDELLTELEQPLAAILAEMEFTGV
 KVDTKRLEQMGEELAQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGTGYSTSADVL
 EKLAGPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTKKVHTRFNQALTQTGRLSSTEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEDEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFESFPGVKRYMENIVQEAKQKGYVTT
 LLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSAADIICKAMIDLAKRLKEERLQARLLLQVHDELI
 LEAPKEEIERLEKLVPVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 9
 AEEEKPLAEMEFAIADSUTEEMLADKAALVVEVVEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 LAWLGDETKKSMFDKRAAVALKWGIELRGVAFDLLAAYLLNPAQAAGDVAAVAKMKQYEAVRSD
 EAVYKGAKRSVPDEPTLAEHLVRKAAAIWALEQPFMDELRRNEQDRLLTELEQPLASILAEMEFTGV
 KVDTKRLEQMGEELTEQLRAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGTGYSTSADVL
 EKLAGPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRLSSTEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFESFPGVKQYMETIVQEAKQKGYVTT
 LLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSAADIICKAMIDLAAARLKEERLQARLLLQVHDELI
 LEAPKEEIERLCRLVPVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 10
 AEDETPLMEMEFVIADGITDEMLADKAALVVEVQEEENYHDAPIVGIALVNEHGRFFLRAEMALADPQF
 VAWLADETKKSMFDKRAAVALKWGIELRGVDFDLLAAYLLNPAQTDDEDVAAVAKMKQYEAVRPD
 EAVYKGAKRPLPDEPALAEHLVRKAAAIWALERPFLDELRSNEQDELLIKLEPLATILAEMEFTGV
 KVDTKRLEQMGEELAQLRAVEQRIYELAGQEFNINSPKQLGIILFEKLQLPVLKKTGTGYSTSADVL
 EKLAGPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRLSSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
 TARMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFESFPGVKRYMETIVQEAKQKGYVTT
 LLHRRRLPDITSRNPNVRSFAERMAMNTPIQGSAADIICKAMIDLAAARLKEERLQARLLLQVHDELI
 LEAPKEEMERLCQLVPVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 11
 AEEEKPLAEMEFTIADDEVTEEMLADKAALVVEVLEENYHDAPIVGIALVNEHGRFFLRPETALADSQF
 LAWLDEDETKKSMFDKRAAVALKWGIELRGVAFDLLAAYLLNPAQAAGDVAAVAKMKQYEAVRSD
 EAVYKGAKRAVPDEPVLAELVRAAAIWALEPPFIDELRRNEQDRLLTDLEQPLSSILAEMEFTGV
 KVDTKRLEQMGEELAEQLRAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGTGYSTSADVL
 EKLAGPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRLSSTEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIANDDNLIEAFRRDLDIHTKTAMDIFHVSEDEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFESFPGVKQYMETIVQEAKQKGYVTT

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LLHRRRYLPDITSRNFNVRSPAERTAMNTPIQGSAADIKKAMIDLARLKEERLQARLLLQVHDELI
LEAPKEEIERLCOLVPEVMEQAVTLRVPLKVDYHYGPTWYDAK

SEQ ID NO: 12
AEEEKPLAEMEFAIADSVTEEMLADKAALVVEVVEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
LAWLGETKKSMFDKRAAVALKWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQEAVRSD
EAVYGKGAKRSPVDEPTLAEHLVRKAAAIWALEQPFMDELRRNEQDRLLTEQPLASILAEMEFTGV
KVDTKRLEQMGEELABQLRAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTMFNQALTQTGRLSSTEPNLQNIPIR
LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLahiADDDNLIEAFRRDLIDIHTKTAMDIFHVSEEEV
TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASPPGVKRYMENIVQEAQKGYVTT
LLHRRRYLPDITSRNFNVRSPAERTAMNTPIQGSAADIKKAMIDLARLKEERLQARLLLQVHDELI
LEAPKEEIERLCOLVPEVMEQAVTLRVPLKVDYHYGPTWYDAK

SEQ ID NO: 13
SEEKPLAKMAFTLADEVTEEMLADKAALVVEVVEENYHDAPIVGIAVVNEHGRFFLRPETALASPQF
VAWLGETKKSMFDKRAIVALWKWKGIELCGVSFDLLLAAAYLLDPAQGVDDAAAAMKQEAVRPD
EAVYGKGAKRAVPDEPVLAEHLVRKAAAIWALERPFLDELRRNEQDRLLTEQPLSSILAEMEFAVG
KVDTKRLEQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTKKVHTRFNQALTQTGRLSSTEPNLQNIPIR
LEEGRKIRQAFVPSEDWLIFAADYSQIELRVLAHIAEDDNLMEAFRRDLDIHTKTAMDIFQVSEDEV
TPNMRRQAKAVNFGIVYGISDYGLAQNLNISRKEAAEFIERYFESPPGVKRYMENIVQEAQKGYVTT
LLHRRRYLPDITSRNFNVRSPAERMAMNTPIQGSAADIKKAMIDLARLKEERLQARLLLQVHDELI
LEAPKEEMERLCOLVPEVMEQAVELRVPLKVDYHYGSTWYDAK

SEQ ID NO: 14
AEEEKPLAEMEFAIDEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALASPQF
VAWLADETKKSMFDAKRAIVALWKWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQEAVRSD
EAVYGKGAKRAVPDEPTLAEHLVRKAAAIWALERPFLDELRRNEQDELLTEQPLATILAEMEFTGV
KVDTKRLEQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTMFNQALTQTGRLSSTEPNLQNIPIR
LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLahiADDDNLIEAFRRDLIDIHTKTAMDIFHVSEEEV
TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASPPGVKRYMENIVQEAQKGYVTT
LLHRRRYLPDITSRNFNVRSPAERTAMNTPIQGSAADIKKAMIDLARLKEERLQARLLLQVHDELI
LEAPKEEIERLCOLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 15
AEEEKPLAEMEFAIADGITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
VAWLADETKKSMFDAKRAAVALKWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQEAVRSD
EAVYGKGAKRAVPDEPTLAEHLVRKAAAIWALERPFLDELRRNEQDELLIKLEQPLATILAEMEFTGV
KVDTKRLEQMGEELAEQLGAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTMFNQALTQTGRLSSTEPNLQNIPIR
LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIAEDDNLIEAFRRDLIDIHTKTAMDIFHVSEEEV
TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASPPGVKRYMENIVQEAQKGYVTT
LLHRRRYLPDITSRNFNVRSPAERTAMNTPIQGSAADIKKAMIDLARLKEERLQARLLLQVHDELI
LEAPKEEIERLCOLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

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SEQ ID NO: 16

EEEEKPLEDISFEIADEVTEMLTDESALVVEVLEENYHKADIVGFAIANENGNFFIPTDTALASPOF
 KWLEDETKKKSVFDAKRAIVALWKWGIELKGVDFDLLIASYLLNPSESSDDFASVAKTKGYNAVQSD
 EAVYGKGAKRAVPDEEKLAEHLARKAAAISALKETFIHELKENEQYELLTELEMLALILADMEYTGV
 KVDVERLKEELTERLKEIEQKIELYLAGQEFNINSPKQLGVILFEKLGLPVIKKTGYSTSADVL
 EKLASHHEIIRHILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRRLSTDPNLQNIPIR
 LEEGRKIRQAFVPSEPGWVIFAADYSQIELRVLVLAHIANDNLIEAFRHDMDIHTKTAMDVFHVSEDEV
 TSNMRQQAKAVNFGIVYGISDYGLSQNLGITRKEAGEFIREYLESFPGVKEYMDDIVQEAKQKGYVTT
 LHRRRYLPDITSRNFNVRSAERTAMNTPIQGSAAIDIKKAMIDLKEENLQARLLLQVHDELI
 FEAPKEEIEKLCKLVPEVMENAVELKVPLKVDYSYGPWTYDAK

SEQ ID NO: 17

ADEEKPLEEIIFAIADEITEEMLADKAALVVEVLEENYHDAPIVGFAIVNEHGRFFIRPETALASSQF
 KAWLEDETKKKSMFDFAKRAAVALWKWGIELRGVAFDLLAAYLLNPAQSAGDVAAVAKMKQEAVRSD
 EAVYGKGAKRAVPDEPTLAEHLVRKAAAIWALEQPPLDELRENEQDELLTKLEQPLALILAEMEFTGV
 KVDTKRLEQMGEELAEQLKEIEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRRLSTEPLNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDVFHVSEEV
 TANMRQQAKAVNFGIVYGISDYGLSQNLNITRKEAAEFIREYFASFPGVKRYMEEIVQEAKQKGYVTT
 LHRRRYLPDITSRNFNVRSAERTAMNTPIQGSAAIDIKKAMIDLKEERLQARLLLQVHDELI
 LEAPKEEIERLCQLVPEVMEQAVTLRVPLKVDYHYGPTWYDAK

SEQ ID NO: 18

AEEEKPLADMEFAIADEVTEEMLADKAALVVEVMEDNYHDAPIVGFANVNEHGRFFLRABLAADSQF
 LAWLEDETKKKSMFDRKRAAVALWKWGIELRGVAFDLLAAYLLNPAQDADDVAAVAKMKQEAVRPD
 EAVYGKGAKRSVPDEPVLAEHLVRKAAAIWALERPFLDELRRNEQDRLLTEQPLATILAEMEFTGV
 KVDTKRLEQMGEELAEQLRAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRRLSTEPLNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDVFHVSEEV
 TARMRRQQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIREYFASFPGVKRYMENIVQEAKQKGYVTT
 LHRRRYLPDITSRNFNVRSAERMAMNTPIQGSAAIDIKKAMIDLKEERLQARLLLQVHDELI
 LEAPKEEIERLCQLVPEVMEQAVTLRVPLKVDYHYGPTWYDAK

SEQ ID NO: 19

AEGEKPLAEMEFAIVDEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPOF
 LAWADETKKKSMFDFAKRAAVALWKWGIELRGVAFDLLAAYLLNPAQDAGDVAAVAKMKQEAVRSD
 EAVYGKGAKRSVPDEPTLAEHLVRKAAAIWALEQPPLDELRRNEQDELLTKLEQPLATILAEMEFTGV
 KVDTKRLEQMGEELAEQLGAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRRLSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDVFHVSEEV
 TANMRQQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIREYFASFPGVKRYMENIVQEAKQKGYVTT
 LHRRRYLPDITSRNFNVRSAERTAMNTPIQGSAAIDIKKAMIDLKEERLQARLLLQVHDELI
 LEAPKEEIERLCQLVPEVMEQAVTLRVPLKVDYHYGPTWYDAK

SEQ ID NO: 20

AEEEKPLEEMEFAIADEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFMRPETALASPOF
 LAWLADETKKKSMFDFAKRAAVALWKWGIELRGVAFDLLAAYLLNPAQDAGDIAAVAKMKQEAVRSD

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EAVYKGKVKRSPLPDEQT LAEHLVRKAAAIWALEQPFMDDLRNNEQDQLLTELEQPLAAILAEMEFTGV
 NVDTKRLEQMGSELAEQLKEIEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTRGLSSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFQRDLDIHTKTAMDIFHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASFPGVKQYMEMIVQEAKQGYVTT
 LLHRRRYLPDITSRNFNVRSPAERTAMNTPIQGSAADI IKKAMIDLAARLKEEQLQARLLLQVHDELI
 LEAPKEEIERLCKLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 21

TEEEKELEDINVKADEVTSEMLTDPSALVVEQLGDNYHEADIIIGFAIVNENGAFFIPKETALQSPQF
 KEWVEDETKKKWFDSKRAIVALRWHGIELKGVDFDVLLASYIIINPSNSYDDVASVKEYGLNIVSSD
 EAVYKGKAKRAVPAEDELAEHLGRAAAISALRDKLLQALEENDQYELLTELEMLALILGEMESTGV
 KVDVERLKRGEELTEKLKEYEKIHELAGEPFNINSPKQLGVILFEKLGLPVIKKTGYSTSADVL
 EKLADKHIIIRYILHYRQIGKLQSTYIEGLLKVVTRKDTHKVHTRFNQALTQTRGLSSTDPNLQNIPIR
 LEEGRKIRQAFVPSEEGWLIFAADYSQIELRVLVLAHSKDNLIEAFTHDMDIHTKTAMDVFHVSEDEV
 TSAMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAGIFIERYLESFPGVKAYMEDIVQEAKQGYVTT
 LLHRRRYIPEITSRNFNIRSPAERTAMNTPIQGSAADI IKKAMIDMAARLKEENLQARLLLQVHDELI
 PEAPKEEIEILCKLVPEVMEHAVELDPLKVDYASGPSWYDAK

SEQ ID NO: 22

AEEEKPLEEMEFAIADEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALASPQF
 KAWLADETKKSMFDKRAIVALWKKGIELRGVAFDLLLAAAYLLNPQAQDAGDVAAVAKMKQYEAVRSD
 EAVYKGKAKRAVDPDETLAEHLVRKAAAIWALERPFLDELRNNEQDELLTELEQPLALILAEMEFTGV
 KVDTKRLEQMGEEELAEQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTRGLSSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAAEFIERYLESFPGVKRYMEMIVQEAKQGYVTT
 LLHRRRYLPDITSRNFNVRSPAERTAMNTPIQGSAADI IKKAMIDLAERLKEEQLQARLLLQVHDELI
 LEAPKEEIERLCKLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 23

EEEEKPLEDISFEIADEVTEEMLTDESALVVEVLEENYHKADIVGFAIVNENGNNFIPTDTALASPQF
 KKWLDEDTKKKTVFDKRAIVALWKKGIELKGVDFDLLIASYLLNPSETNDDFASVAKTKGYNAVQSD
 EAVYKGKAKRAVPEEKLAELKAAAIKETFIQELKENEQYELLTELEMLALILADMEYFTGV
 KVDVERLKEMGEELAERLKEIEQKIYELAGEEFNINSPKQLGVILFEKLGLPVIKKTGYSTSADVL
 EKLASKHEIIRNILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTRGLSSTDPNLQNIPIR
 LEEGRKIRQAFVPSEEGWVIPAADYSQIELRVLVLAHIANDEKLIEAFRHDMIHTKTAMDVFHVSEDEV
 TSNMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAAEFIERYLESFPGVKEYMDDIVQEAKQGYVTT
 LLHRRRYLPDITSRNFNLRSPAERTAMNTPIQGSAADI IKKAMIDMANRLKEENLQARLLLQVHDELI
 PEAPKEEIEKCKKIVPEVMEHAVELKPLKVDYSYGPTWYDAK

SEQ ID NO: 24

AEEEKPLAEMEFAIADEVTEEMLADKAALVVEVVEENYHDAPIVGIALVNEHGRFFLRPETALASPQF
 LAWLGDDETKKSMFDKRAIVALWKKGIELRGVAFDLLLAAAYLLNPQAAGDVAAVAKMKQYEAVRSD
 EAVYKGKAKRSVPDETLAEHLVRKAAAIWALEQPFMDELRRNEQDRLLTELEQPLASILAEMEFTGV
 KVDTKRLEQMGEEELTEQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTRGLSSTEPNLQNIPIR

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LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASPPGVKRYMENIVQEAKQKGYVTT
 LLHRRRLPDISRNFNVRSPAERTAMNTPIQGSAADI IKKAMIDLAARLKEERLQARLLLQVHDELI
 LEAPKEEIERLCKLVPVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 25
 AEEEVPLEEMEFTIADEITEEMLADKAALVVEVLEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 VAWLEDETKKSMFDAKRAAVALKWKGIELRGVAFDLLAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYGKGAKRSLPDEPVLAELVRAAAIWALERPFLDELRENEQDELLTDLEQPLSSILAEMEFTGV
 KVDTKRLEQMGEELAEQLRAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTIFNQALTQTGRLSSTEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFESPPGVKRYMENIVQEAKQKGYVTT
 LLHRRRLPDISRNPNVRSFAERTAMNTPIQGSAADI IKKAMIDLAARLKEERLQARLLLQVHDELI
 LEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 26
 AEEEAPLEDIEFDIADEVTEEMLADKAALVVEVQEDNYHDAPIVGFAIVNEHGRFFIRTELASEAF
 KAWLADETKKSVFDAKRAIVALWKWKGIELRGVDFDLLAAYLLNPAQTADDVAAVAKMKQYHAVRSD
 EAVYGKGAKRAVPDEPVLAELVRAAAIWALEEPFLDELRKNEQDELFTELEPLALILAEMEFTGV
 KVDTKRLEQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTRFNQALTQTGRLSSTDPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDVHVSEDEV
 TSNMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAAEFIERYFESPPGVKEYMEDIVQEAKQKGYVTT
 LLHRRRLPDISRNFNLRSPAERTAMNTPIQGSAADI IKKAMIDMAARLKEERLQARLLLQVHDELI
 FEAPKEEIERLEKLVPVMEHAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 27
 AEEEVPLEEMEFTIADEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRAETALADPQF
 VAWLADETKKSMFDAKRAAVALKWKGIELRGVAFDLLAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYGKGAKRSLPDEPTLAEHLVRAAAIWALERPFLDELRENEQDELLIKLEQPLATILAEMEFTGV
 KVDTKRLEQMGEELAEQLRAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTMFNQALTQTGRLSSTEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASPPGVKRYMENIVQEAKQKGYVTT
 LLHRRRLPDISRNFNVRSPAERTAMNTPIQGSAADI IKKAMIDLAARLKEERLQARLLLQVHDELI
 LEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 28
 EEEEKPLAKIAFTLADRVTDEMLADKAALVVEVVEDNYHDAPIVGIAVVNEHGRFFLRPETALADPQF
 VAWLGDETKKSVFDSKRAAVALKWKGIELCGVSFDLLAAYLLDPAQGVDDVAAAAMKQYHAVRPD
 EAVYGKGAKRAVPDEPVLAELVRAAAIWALERPFLDELRRNEQDRLLVELEQPLSSILAEMEFGAV
 KVDTKRLEQMGEELAEQLKEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTKVKVHTIFNQALTQTGRLSSTEPNLQNIPIR
 LEEGRKIRQAFVPSESDWLIFAADYSQIELRVLVLAHIAEDENLMEAFRRDLDIHTKTAMDIQVSEDEV
 TPNMRRQAKAVNFGIVYGISDYGLSQNLGISRKEAAEFIERYFESPPGVKRYMENIVQEAKQKGYVTT

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LLHRRRYDPDITSRNFNVRSAERMAMNTPIQGSAADI IKKAMIDLNLARLKEERLQARLLLQVHDELI
LEAPKEEMERLCRLVPEVMEQAVTLRVLKVDYHYGSTWYDAK

SEQ ID NO: 29

AEEEKPLAEMEFAIADEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADSQF
LAWLADETKKSMFDAKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
EAVYKGAKRSVPDEPTLAEHLVRKAAAIWALEQPFDELRRNEQDRLLTKEQPLATILAEMEFTGV
KVDTKRLEQMGSELAEQLRAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGTGYSTSADVL
EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTMFNQALTQTGRLSSTEPNLQNIPIR
LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASFPGVKRYMENIVQEAKQKGYVTT
LLHRRYLPDITSRNFNVRSAERTAMNTPIQGSAADI IKKAMIDLNLARLKEERLQARLLLQVHDELI
LEAPKEEIERLCQLVPEVMEQAVTLRVLKVDYHYGPTWYDAK

SEQ ID NO: 30

AEEEVPLAEMEFAIADEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
LAWLADETKKSMFDAKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
EAVYKGAKRSVPDEPTLAEHLVRKAAAIWALERPFLDELRRNEQDELLTKEQPLATILAEMEFTGV
KVDTKRLEQMGSELAEQLRAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGTGYSTSADVL
EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTMFNQALTQTGRLSAEPNLQNIPIR
LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASFPGVKRYMENIVQEAKQKGYVTT
LLHRRYLPDITSRNFNVRSAERTAMNTPIQGSAADI IKKAMIDLNLARLKEERLQARLLLQVHDELI
LEAPKEEIERLCQLVPEVMEQAVTLRVLKVDYHYGPTWYDAK

SEQ ID NO: 31

AEDEKPLAEMEFAIDGITDEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
VAWLADETKKSMFDAKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRPD
EAVYKGAKRSVPDEPTLAEHLVRKAAAIWALERPFLDELRRNEQDRLLIKLEQPLATILAEMEFTGV
KVDTKRLEQMGSELAEQLRAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGTGYSTSADVL
EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTMFNQALTQTGRLSAEPNLQNIPIR
LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASFPGVKRYMENIVQEAKQKGYVTT
LLHRRYLPDITSRNFNVRSAERTAMNTPIQGSAADI IKKAMIDLNLARLKEERLQARLLLQVHDELI
LEAPKEEMERLCRLVPEVMEQAVTLRVLKVDYHYGPTWYDAK

SEQ ID NO: 32

EEEEEPLEDISFEIVEEVTEEMLTDESALVVEVLEENYHKADIVGFAIVNENGNNFFIPTDTALASEAF
KWKLEDETKKTVFDAKRAIVALWKGIELKGVDFDLLIASYLLNPSETNDDFASVAKTKGYNNAVQSD
EAVYKGAKRAVPEEKLAELHARKAAAISALKETFIQELKENEQYELFTDLEMLALILADMEYFTGV
KVDVERLKEMGEELAERLKEIEQKIYELAGEEFNINSPKQLGVILFEKLGLPVIKKKTGTGYSTSADVL
EKLASKHEIIRNILHYRQLGKLQSTYIEGLLKVVHQDTGVHTRFNQALTQTGRLSSTDPNLQNIPIR
LEEGRKIRQAFVPSEEGWVIFAADYSQIELRVLVLAHIANDEKLIEAFRHMDIHTKTAMDVFHVSEDEV
TSNMRRQAKAVNFGIVYGISDYGLSQLGILTKEAAIFIERYLESFPGVKEYMDDIVQEAKQKGYVTT
LLHRRYLPDITSRNFNLRSAERTAMNTPIQGSAADI IKKAMIDMANRLKEENLQARLLLQVHDELI
FEAPKEEIEKLKKIVPEVMEHAVELKVLKVDYSYGPTWYDAK

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SEQ ID NO: 33
AEKELPLMEMEFADADTITMEMLADKAALVVEVMEENYHDAPIVGIANVNEHGRFFLRTELALADPQF
VAWLEDETKKSMFDRKRAAVALWKGIELGVDFDLLAAYLLAPAQDDGDAAAKAKMKQYEAVRED
EAVYGKGAKRDPDELAELAEHVLRAAAIWALERPFLDELRENEQDLLLLEQPLILILAEMEFTGV
DVDTKRLEQMGEELABQLVEQEORIYELAGQEFNINSPKQLGLILFEKLQLPVLKKTGYSTSADVL
EKLAPEHEIVENILHYRQLGKLQSTYIEGLLKVVDTGKVHTMFNQALTQTGRLSSAEPNLQNIPIR
LEEGRKIRQAFVPSEPLWLIFAADYSQIELRVLIAHIAEDDNLAEAFRRDLDIHTKTAMDIFHVSEEEV
TARMRRQAKAVNFGIVYGISDYGLAQNLNKRKEAAEFIERYFESFPGVKRYMEVIVQEAKQKGYVTT
LLHRRRYLPDITSRNFNVRSFAERMAMNTPIQGSAADI IKKAMIDLARLKEEQLQARLLLQVHDELI
LEAPKEEMERLCVLVPEVMEQAVRLRVPLKVDYHYGWTWYDAK

SEQ ID NO: 34
SEEKPLAKIAFDLADRVTTEMLADKAALVVEVQEDNYHDAPIVGIAVVNEHGRFFLRTELALASPOF
VAWLGETKKSMFDSKRAIVALWKGIELCGVDFDLLAAYLLPAQTDAAAQAKAKMKQYHAVRPD
EAVYGKGAKRAVPDEPVLAELAEHVLRAAAIWALEEPFLDELRRNEQDRLLIEEMPLSSILAEMEFAVG
KVDTKRLEQMGEELAEQLRTVEQRIYELAGQEFNINSPKQLGLILFEKLQLPVLKKTGYSTSADVL
EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTKVKVHTIFNQALTQTGRLSSTEPNLQNIPIR
LEEGRKIRQAFVPSESDWLIFAADYSQIELRVLIAHIAEDDNLMEAFRDLDIHTKTAMDVFQVSEDEV
TPRMRRQAKAVNFGIVYGISDYGLSQNLGIISRKKEAAIFIERYFESFPGVKRYMENIVQEAKQKGYVTT
LLHRRRYLPDITSRNFNVRSFAERMAMNTPIQGSAADI IKKAMIDLNRALKERLQARLLLQVHDELI
LEAPKEEMERLCRLVPEVMEQAVTLRVPLKVDYHYGSTWYDAK

SEQ ID NO: 35
AEEEKPLEEMEFAIADEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALASPOF
KAWLADETKKSMFDAKRAIVALWKGIELRGVAFDLLAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
EAVYGKGAKRAVPDEPVLAELAEHVLRAAAIWALERPFLDELRNNEQDELLTEQPLAAILAEMEFTGV
KVDTKRLEQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTMFNQALTQTGRLSSTEPNLQNIPIR
LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLIAHIAEDDNLIEAFRRDLDIHTKTAMDIFHVSEDEV
TANMRRQAKAVNFGIVYGISDYGLSQNLNITRKKEAAIFIERYFESFPGVKRYMENIVQEAKQKGYVTT
LLHRRRYLPDITSRNFNVRSFAERTAMNTPIQGSAADI IKKAMIDLARLKEERLQARLLLQVHDELI
LEAPKEEIERLCKLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 36
AEEEKPLEDIEFEIADEVTEEMLADEAALVVEVLEENYHDAPIVGFALVNEHGRFFIRTELASSQF
KAWLEDETKKSVFDAKRAIVALWKGIELRGVDFDLLAAYLLNPAQSAGDVAAVAKMKQYEAVRSD
EAVYGKGAKRAVPDEPTLAEHVLRAAAIWALEEPFIDELRENEQDELFTEEMPLALILAEMEFTGV
KVDTKRLEQMGEELAEQLKAI EQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHTMFNQALTQTGRLSSTEPNLQNIPIR
LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLIAHIANDENLIEAFRRDLDIHTKTAMDIFHVSEDEV
TANMRRQAKAVNFGIVYGISDYGLSQNLNITRKKEAAIFIERYFESFPGVKQYMEDIVQEAKQKGYVTT
LLHRRRYLPDITSRNFNVRSFAERTAMNTPIQGSAADI IKKAMIDLARLKEERLQARLLLQVHDELI
LEAPKEEIERLCKLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 37
AEEEKPLAEMEFVIADEITDEMADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALASPOF
VAWLADETKKSMFDAKRAIVALWKGIELRGVAFDLLAAYLLNPAQDAGDVAAVAKMKQYEAVRPD

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EAVYKGAKRSLPDEPTLAEHLLVRKAAAIWALERPFLDELRRNEQDRLLTEQPLATILAEMEFTGV
 KVDTKRLEQMGSELAEQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRLSSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASFPGVKRYMENIVQEAKQGYVTT
 LLHRRYLPDITSRNFNVRSAERTAMNTPIQGSAAIDIKKAMIDLARLKEERLQARLLLQVHDELI
 LEAPKEEMERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 38
 AEGEKPLAEMEFAIVDEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 LAWLADETKKKSMFDAKRAIVALWKIGIELRGVAFDLLAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYKGAKRSLPDEPTLAEHLLVRKAAAIWALEQPFIDELRRNEQDELLTKEQPLATILAEMEFTGV
 KVDTKRLEQMGSELAEQLGAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRLSSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASFPGVKRYMENIVQEAKQGYVTT
 LLHRRYLPDITSRNFNVRSAERTAMNTPIQGSAAIDIKKAMIDLARLKEERLQARLLLQVHDELI
 LEAPKEEIERLCQLVPEVMEQAVTLRVLKVDYHYGPTWYDAK

SEQ ID NO: 39
 AEEEKPLAEMEFAIADEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 KAWLADETKKKSMFDAKRAIVALWKIGIELRGVDFDLLAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYKGAKRALPDEPTLAEHLLVRKAAAIWALEEPFLDELRENEQDELLTEQPLALILAEMEFTGV
 KVDTKPLEQMGEEELAEQLKAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRLSSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASFPGVKRYMEDIIVQEAKQGYVTT
 LLHRRYLPDITSRNFNVRSAERTAMNTPIQGSAAIDIKKAMIDLARLKEERLQARLLLQVHDELI
 LEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 40
 AEDEKPLAEMEFAIADGITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 LAWLADETKKKSMFDAKRAAVALWKIGIELRGVAFDLLAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYKGAKRSLPDEPTLAEHLLVRKAAAIWALEQPFMDELRSNEQDQLLTKEQPLASILAEMEFTGV
 KVDTKRLEQMGSELAEQLRAVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL
 EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTRFNQALTQTGRLSSAEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSEEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFASFPGVKQYMEMENIVQEAKQGYVTT
 LLHRRYLPDITSRNFNVRSAERTAMNTPIQGSAAIDIKKAMIDLARLKEERLQARLLLQVHDELI
 LEAPKEEIERLCQLVPEVMEQAVTLRVLKVDYHYGPTWYDAK

SEQ ID NO: 41
 AEEEKPLEEMEFAIADEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 LAWLADETKKKSMFDAKRAAVALWKIGIELRGVAFDLLAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYKGAKRVPDEPVLAEHLVRKAAAIWALERPFLDELRRNEQDELLTEQPLATILAEMEFTGV
 KVDTKRLEQMGEEELAEQLKEVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTGYSTSADVL

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EKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHTMFNQALTQTGRLSSTEPNLQNIPIR
 LEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNLIEAFRRDLDIHTKTAMDIFHVSSEEV
 TANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYFESFPGVKRYMENIVQEAKQKGYVTT
 LLHRRRLPDISRNFNVRSAERTAMNTPIQGSAADIKKAMIDLAARLKEERLQARLLLQVHDELI
 LEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 42

EEEEEPLEDISFEIVEEVTEDMLTDESALVVEVLEENYHKADIVGFAIANENGNNFIPTDTALASEAF
 KKWLEDETKKSVFDAKRAIVALKWHGIELKGVDFDLLIASYLLNPSESSDFASVAKTKGYNAVQSD
 EAVYGKGAKRAVPDEEKLAELARKAAAISALKETFIHELKENEQYELFTDLEMLPLALILADMEYTGV
 KVDVERLKEMGEELTERLKEIEQKUYELAGQEFNINSPKQLGVILFEKGLPVIKKTKGYSTSADVL
 EKFLASHHEIIRHILHYRQLGKLQSTYIEGLLKVVHEDTGKVHTMFNQALTQTGRLSSTDPNLQNIPIR
 LEEGRKIRQAFVPSEPGWVIFAADYSQIELRVLVLAHIANDNLIEAFRHMDIHTKTAMDVFHVSSEDEV
 TSNMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAGEFIERYLESFPGVKEYMDDIVQEAKQKGYVTT
 LLHRRRLPDISRNFNVRSAERTAMNTPIQGSAADIKKAMIDMADRKEENLQARLLLQVHDELI
 FEAPKEEIEKLKKIVPEVMENAVELKVPLKVDYSYGPWTWYDAK

SEQ ID NO: 43

EQDRLLTELEQPLASILAEMEFTGVNVDTKRL_EQMGSELAEQLKEQEQRUYELAGQEFNINSPKQLGV
 ILFEKQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHT
 RFNQALTQTGRSSAEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNL
 EAQRDLDIHTKTAMDIFHVSSEEVETANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYF
 ASFPGVKEYMENIVQEAKQKGYVTTLLHRRRLPDISRNFNVRSAERTAMNTPIQGSAADIKKAM
 IDLAARLKEEQLQARLLLQVHDELIPEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 44

EQYELLTELEMLALILADMEYTGVKVDVERLKEMGEELTERLKEIEQKUYELAGQEFNINSPKQLGV
 ILFEKGLPVIKKTKGYSTSADVLEKLASHHEIIRHILHYRQLGKLQSTYIEGLLKVVHPDTGVHT
 RFNQALTQTGRSSAEPNLQNIPIRLEEGRKIRQAFVPSEPGWVIFAADYSQIELRVLVLAHIANDNL
 EAFRHMDIHTKTAMDVFHVSSEDEVTSNMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAGEFIERYL
 ESFPGVKEYMDDIVQEAKQKGYVTTLLHRRRLPDISRNFNVRSAERTAMNTPIQGSAADIKKAM
 IDMADRKEENLQARLLLQVHDELIPEAPKEEIEKLCKLVPEVMENAVELKVPLKVDYSYGPWTWYDAK

SEQ ID NO: 45

EQDELFKLEQPLATILAEMEFTGVKVDTKRL_EQMGSELAEQLKEVEQRUYELAGQEFNINSPKQLGV
 ILFEKQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHT
 RFNQALTQTGRSSAEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSSEEVETANMRRQAKAVNFGIVYGISDYGLAQNLNIRKEAAEFIERYF
 ASFPGVKRYMENIVQEAKQKGYVTTLLHRRRLPDISRNFNVRSAERTAMNTPIQGSAADIKKAM
 IDLAARLKEERLQARLLLQVHDELIPEAPKEEIERLEQLVPEVMEQAVRLRVPLKVDYHYGPTWYDAK

SEQ ID NO: 46

EQDELLTELEQPLALILAEMEFTGVKVDTKRL_EQMGEEELAEQLKEVEQRUYELAGQEFNINSPKQLGV
 ILFEKQLPVLKKTGTGYSTSADVLEKLAPHREIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHT
 RFNQALTQTGRSSAEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSSEEVETANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYF
 QSFPGVKRYMEDIIVQEAKQKGYVTTLLHRRRLPDISRNFNVRSAERTAMNTPIQGSAADIKKAM
 IDLAARLKEERLQARLLLQVHDELIPEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYRYGPTWYDAK

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SEQ ID NO: 47

EQDELFTELELPLALILAEMEFTGVKVDTKRL_EQMGSELAEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 RFNQALTQTGRLLSSTDPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRRDMDIHTKTAMDVFHVSEDEVTSNMRROAKAVNFGIVYGISDYGLSQNLGITRKEAAEFIERYF
 ESFPGVKEYMEDIVQEAKQKGVTLLHRRRYLPDITSRNPNVRSFAERTAMNTPIQGSAADIKKAM
 IDLAARLKEERLQARLLLQVHDELILEAPKEEIERLECLVPEVMHAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: NO: 48

EQDRLLTELEQPLATILAEMEFTGVKVDTKRL_EQMGSELAEQLRAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 RFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRRDLDIHTKTAMDVFHVSEEVETARMRRQAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ASFPGVKRYMENIVQEAKQKGVTLLHRRRYLPDITSRNPNVRSFAERMAMNTPIQGSAADIKKAM
 IDLAARLKEERLQARLLLQVHDELILEAPKEEIERLCQLVPEVMQAVTLRVPBKVDYHYGPTWYDAK

SEQ ID NO: 49

EQDQLLTELEQPLAAILAEMEFTGVNVDTKRL_EQMGSELAEQLKEIEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 RFNQALTQTGRLLSSEAPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAQRDLIDIHTKTAMDIFHVSEEEVTANMRROAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ASFPGVKQYMFENIVQEAKQKGVTLLHRRRYLPDITSRNPNVRSFAERTAMNTPIQGSAADIKKAM
 IDLAARLKEEQLQARLLLQVHDELILEAPKEEIERLCQLVPEVMQAVELRVPBKVDYHYGPTWYDAK

SEQ ID NO: 50

EQDELLTELEQPLATILAEMEFTGVKVDTKRL_EQMGSELAEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 RFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRRDLDIHTKTAMDIFHVSEEEVTANMRROAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ASFPGVKRYMENIVQEAKQKGVTLLHRRRYLPDITSRNPNVRSFAERTAMNTPIQGSAADIKKAM
 IDLAARLKEERLQARLLLQVHDELILEAPKEEIERLCQLVPEVMQAVELRVPBKVDYHYGPTWYDAK

SEQ ID NO: 51

EQDQLLTKLEQPLASILAEMEFTGVKVDTKRL_EQMGSELAEQLRAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSSEAPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRRDLDIHTKTAMDIFHVSEEEVTANMRROAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ASFPGVKQYMFENIVQEAKQKGVTLLHRRRYLPDITSRNPNVRSFAERTAMNTPIQGSAADIKKAM
 IDLAARLKEERLQARLLLQVHDELILEAPKEEIERLCQLVPEVMQAVELRVPBKVDYHYGPTWYDAK

SEQ ID NO: 52

EQDELLTELEQPLATILAEMEFTGVKVDTKRL_EQMGSELAEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRRDLDIHTKTAMDIFHVSEEEVTANMRROAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ESFPGVKRYMENIVQEAKQKGVTLLHRRRYLPDITSRNPNVRSFAERTAMNTPIQGSAADIKKAM
 IDLAARLKEERLQARLLLQVHDELILEAPKEEIERLCQLVPEVMQAVELRVPBKVDYHYGPTWYDAK

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SEQ ID NO: 53
 EQDRLLTELEQPLATILAEMEFTGVKVDTKRLEQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 RFNQALTQTGRLLSAEPNLQNIPIRLEEGRKIRQAQFVSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRRQAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ASFPGVKRYMENIVQEAQKGYTTLLHRRRLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELIPEAPKEEMERLCKLVPVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 54
 DQYELLTELEMLPLALILGEMESTGVKVDVERLKRMEELTEKLKEYEEKIHELAGEPFNINSPKQLGV
 ILFEKLGLPVIKKTKTGYSTSADVLEKLADKHEIIRYILHYRQIGKLQSTYIEGLLKVTRDTHKVHT
 RFNQALTQTGRLLSDPNLQNIPIRLEEGRKIRQAQFVSEEGWLIFAADYSQIELRVLAHISKDENLI
 EAFTHDMDIHTKTAMDVFHVSEDEVTSAMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAGAFIERYL
 ESFPGVKAYMEDIVQEAQKGYTTLLHRRRLPEITSRNFNIRSFAERTAMNTPIQGSAADIIKKAM
 IDMAARLKEENLQARLLQVHDELIPEAPKEEIEILCKLVPVMEHAVELVPLKVDYASGPWSYDAK

SEQ ID NO: 55
 EQYELLTELEMLPLALILADMEYTGVKVDVERLKEMGEELAERLKEIEQKIELAGEEFNINSPKQLGV
 ILFEKLGLPVIKKTKTGYSTSADVLEKLASKHEIRNILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 RFNQALTQTGRLLSDPNLQNIPIRLEEGRKIRQAQFVSEEGWVIFAADYSQIELRVLAHIANDEKLI
 EAFRHDMDIHTKTAMDVFHVSEDEVTSAMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAAEFIERYL
 ESFPGVKEYMDDIVQEAQKGYTTLLHRRRLPEITSRNFNLRSAERTAMNTPIQGSAADIIKKAM
 IDMANRLKEENLQARLLQVHDELIPEAPKEEIEKCKIVPEVMEHAVELVPLKVDYSYGPTWYDAK

SEQ ID NO: 56
 EQDRLLTELEQPLASILAEMEFTGVKVDTKRLEQMGEELTEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 RFNQALTQTGRLLSTEPNLQNIPIRLEEGRKIRQAQFVSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRRQAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ASFPGVKQYMEMENIVQEAQKGYTTLLHRRRLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELIPEAPKEEIERLCKLVPVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 57
 EQDRLLVELEMLSSILAEMEFTGVKVDTKRLEQMGEELAEQLRTVEQRIYELAGQEFNINSPKQLGL
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTKKVHT
 IFNQALTQTGRLLSTEPNLQNIPIRLEEGRKIRQAQFVSESDWLIFAADYSQIELRVLAHIAEDDNLM
 EAFRDLDIHTKTAMDVFQVSEDEVTPRMRRQAKAVNFGIVYGISDYGLSQNLGIRKEAAEFIERYF
 ESFPGVKRYMENIVQEAQKGYTTLLHRRRLPDITSRNFNVRSAERMAMNTPIQGSAADIIKKAM
 IDLNARLKEERLQARLLQVHDELIPEAPKEEMERLCRLVPVMEQAVTLRVPLKVDYHYGSTWYDAK

SEQ ID NO: 58
 EQDELLTELEQPLALILAEMEFTGVKVDTKRLEQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSAEPNLQNIPIRLEEGRKIRQAQFVSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRRQAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ASFPGVKRYMENIVQEAQKGYTTLLHRRRLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELIPEAPKEEIERLCKLVPVMEQAVELRVPLKVDYHYGPTWYDAK

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SEQ ID NO: 59
 EQDELLTDLEQPLSSILAEMEFTGVKVDTKRLEQMGEELAEQLRAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 IFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAQFVSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEEVTANMRRQAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ESFPGVKRYMENIVQEAQKGYTTLLHRRRLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELILEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 60
 EQDELLIKLEQPLATILAEMEFTGVKVDTKRLEQMGEELAEQLRAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAQFVSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEEVTANMRRQAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ASFPGVKRYMENIVQEAQKGYTTLLHRRRLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELILEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 61
 EQDELLTKLEQPLATILAEMEFTGVKVDTKRLEQMGEELAEQLGAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSAAEPNLQNIPIRLEEGRKIRQAQFVSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEEVTANMRRQAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ASFPGVKRYMENIVQEAQKGYTTLLHRRRLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELILEAPKEEIERLCQLVPEVMEQAVTLRVPLKVDYHYGPTWYDAK

SEQ ID NO: 62
 EQDRLLTDLEQPLSSILAEMEFTGVKVDTKRLEQMGEELAEQLRAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 IFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAQFVSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEDEVTSNMRQAKAVNFGIVYGISDYGLAQNLTTRKEAAEFIERYF
 ESFPGVQYMMENIVQEAQKGYTTLLHRRRLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELILEAPKEEIERLCQLVPEVMEQAVTLRVPLKVDYHYGPTWYDAK

SEQ ID NO: 63
 EQYELFTDLEMLALILADMETYGVKVDVERLKEELTERLKEIEQKIYELAGQEFNINSPKQLGV
 ILFEKLQLPVIKKKTGTGYSTSADVLEKLASHHEIRHILHYRQLGKLQSTYIEGLLKVVHEDTGKVHT
 RFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAQFVSEPGWVIFAADYSQIELRVLAHIADDNL
 EAFRHMDIHTKTAMDVFHVSEDEVTSNMRQAKAVNFGIVYGISDYGLSQNLGITRKEAGEFIERYL
 ESFPGVKEYMDIVQEAQKGYTTLLHRRRLPEITSRNFNLRSAERTAMNTPIQGSAADIIKKAM
 IDMADRKEENLQARLLQVHDELILEAPKEEIEKLKKIVPEVMENAVELKVPLKVDYSYGPWTWYDAK

SEQ ID NO: 64
 EQDELLTELEQPLAAILAEMEFTGVKVDTKRLEQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 RFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAQFVSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEDEVTSNMRQAKAVNFGIVYGISDYGLSQNLNITRKEAAEFIERYF
 ESFPGVKRYMENIVQEAQKGYTTLLHRRRLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELILEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

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SEQ ID NO: 65
 EQDRLLIKLEQPLATILAEMEFTGVKVDTKRLEQMGEELAEQLRAVEQRIFYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSAEPNLQNIPIRLEEGRKIRQAFTPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRQAKAVNFGIVYGISDYGLAQNLTNITRKEAAEFIERYF
 ASFPGVKRYMENIVQEAKQKGYVTTLLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSADIICKAM
 IDLAARLKEERLQARLLQVHDELIAPKEEMERLCRLVPEVMEQAVTLRVPBKDYHYGPTWYDAK

SEQ ID NO: 66
 DQYELFDEMLPLALILGEMESTGVKVDVERLKRMEELTEKLKEYEEKIHELAGEPFNINSPKQLGV
 ILFEKLGLPVIKKTGTGYSTSADVLEKLADKHEIIRYILHYRQIGKLQSTYIEGLLKVTBKDTKVHT
 MFNQALTQTGRLLSDPNLQNIPIRLEEGRKIRQAFTPSEEGWLIFAADYSQIELRVLAHISKDENL
 EAFTHDMDIHTKTAMDIFHVSEDEVTSAMRQAKAVNFGIVYGISDYGLSQNLGITRKEAGAFIERYL
 ASFPGVKAYMEDIVQEAKQKGYVTTLLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSADIICKAM
 IDMAARLKEENLQARLLQVHDELIAPKEEIEILEKIVPEVMEHALELDVPLKVDYASGPSWYDAK

SEQ ID NO: 67
 EQDRLLTKLEQPLATILAEMEFTGVKVDTKRLEQMGEELAEQLRAVEQRIFYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSTEPNLQNIPIRLEEGRKIRQAFTPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRQAKAVNFGIVYGISDYGLAQNLTNITRKEAAEFIERYF
 ASFPGVKRYMENIVQEAKQKGYVTTLLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSADIICKAM
 IDLAARLKEERLQARLLQVHDELIAPKEEIERLCQLVPEVMEQAVTLRVPBKDYHYGPTWYDAK

SEQ ID NO: 68
 EQDELLTKLEQPLALILAEMEFTGVKVDTKRLEQMGEELAEQLKEIEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSTEPNLQNIPIRLEEGRKIRQAFTPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRQAKAVNFGIVYGISDYGLSQNLGITRKEAAEFIERYF
 ASFPGVKRYMEEIVQEAKQKGYVTTLLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSADIICKAM
 IDLAARLKEERLQARLLQVHDELIAPKEEIERLCQLVPEVMEQAVELRVPBKDYHYGPTWYDAK

SEQ ID NO: 69
 EQPLSSILAEMEFAVGKVDTKRLEQMGEELAEQLKEEQRIYELAGQEFNINSPKQLGVILFEKLQLP
 VLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTKVKHTIFNQALTQT
 GRLSSTEPNLQNIPIRLEEGRKIRQAFTPSEPDWLIFAADYSQIELRVLAHIAEDENLMEAFRDLDI
 HTKTAMDIFQVSEDEVTPNMRRQAKAVNFGIVYGISDYGLSQNLGISRKEEAEFIERYFESFPGVKRY
 MENIVQEAKQKGYVTTLLHRRRLPDITSRNPNVRSFAERMAMNTPIQGSADIICKAMIDLNARLKE
 ERLQARLLQVHDELIAPKEEMERLCRLVPEVMEQAVTLRVPBKDYHYGPTWYDAK

SEQ ID NO: 70
 EQDELLIKLEQPLATILAEMEFTGVKVDTKRLEQMGEELAEQLGAVEQRIFYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSTEPNLQNIPIRLEEGRKIRQAFTPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRQAKAVNFGIVYGISDYGLAQNLTNITRKEAAEFIERYF
 ASFPGVKRYMENIVQEAKQKGYVTTLLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSADIICKAM
 IDLAARLKEERLQARLLQVHDELIAPKEEIERLCQLVPEVMEQAVELRVPBKDYHYGPTWYDAK

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SEQ ID NO: 71
 EQDRLLTELEQPLSSILAEMEFAGVKVDTKRL_EQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPYHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTKKVHT
 RFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAFVPSESDWLIFAADYSQIELRVLAHIAEDDNLM
 EAFRDLDIHTKTAMDIFQVSEDEVTPNMRRQAKAVNFGIVYGISDYGLAQNLNISRKEAAEFIERYF
 ESFPGVKRYMENIVQEAQKGYTTLLHRRRYLPDITSRNFNVRSAERMAMNTPIQGSAADIIKKAM
 IDLARLKEERLQARLLQVHDELIPEAPKEEMERLCKLVPEVMEQAVELRVPLKVDYHYGSTWYDAK

SEQ ID NO: 72
 EQDELLTKLEQPLATILAEMEFTGVKVDTKRL_EQMGEELAEQLRAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHT
 MFNQALTQTGRLLSAAEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYF
 ASFPGVKRYMENIVQEAQKGYTTLLHRRRYLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELIPEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 73
 EQDELFDTLEQPLALILAEMEFTGVKVDTKRL_EQMGEELAEQLKEIEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHT
 RFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRRQAKAVNFGIVYGISDYGLSQNLNITRKEAAEFIERYF
 ASFPGVQYMFENIVQEAQKGYTTLLHRRRYLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELIPEAPKEEIERLCQLVPEVMEQAVELRVPLKVDYHYGPTWYDAK

SEQ ID NO: 74
 EQDELFTELELPLALILAEMEFTGVKVDTKRL_EQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHREIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHT
 RFNQALTQTGRLLSTDPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDMDIHTKTAMDIFHVSEEVTANMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAAEFIERYF
 QSFPGVKEYMEDIVQEAQKGYTTLLHRRFLPEITSRNFNLRSAERTAMNIPIQGSAADIIKKAM
 IDMAARLKEERLQARLLQVHDELIPEAPKEEIERLEKLVPEVMEHAVELRVPLKVDYRYGPTWYDAK

SEQ ID NO: 75
 EQDLLLLEQPLILILAEMEFTGVKVDTKRL_EQMGLELAEQLVEQEQRUYELAGQEFNINSPKQLGL
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPEHEIVENILHYRQLGKLQSTYIEGLLKVVDTDTGVHT
 MFNQALTQTGRLLSAAEPNLQNIPIRLEEGRKIRQAFVPSEPLWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTARMRQAKAVNFGIVYGISDYGLAQNLNIRKEAAEFIERYF
 ASFPGVKRYMEIVQEAQKGYTTLLHRRRYLPDITSRNFNVRSAERMAMNTPIQGSAADIIKKAM
 IDLAARLKEEQLQARLLQVHDELIPEAPKEEMERLCVLVPEVMEQAVRLRVPLKVDYHYGWTWYDAK

SEQ ID NO: 76
 EQDELLTELELPLALILAEMEFTGVKVDTKRL_EQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGVHT
 RFNQALTQTGRLLSTDPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDMDIHTKTAMDIFHVSEEVTANMRRQAKAVNFGIVYGISDYGLSQNLGITRKEAAEFIERYF
 ESFPGVKEYMEDIVQEAQKGYTTLLHRRFLPEITSRNFNLRSAERTAMNTPIQGSAADIIKKAM
 IDMAARLKEERLQARLLQVHDELIPEAPKEEIERLCVLVPEVMEHAVELRVPLKVDYHYGPTWYDAK

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SEQ ID NO: 77
 EQDELFTEEMPLALILAEMEFTGVKVDTKRL_EQMGEELAEQLKAIEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIANDENLI
 EAFRDLDIHTKTAMDIFHVSEDEVNTANMRQAKAVNFGIVYGISDYGLSQNLNITRKEAAEFIERYF
 ESFPGVKQYMEDIVQEAKQKGVTLLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSAADIICKAM
 IDLAARLKEERLQARLLQVHDELILEAPKEEIERLCKLVPEVMEQAVELRVLKVDYHYGPTWYDAK

SEQ ID NO: 78
 EQDELLTKLEQPLATILAEMEFTGVKVDTKRL_EQMGEELAEQLGAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSAAEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYF
 ASFPGVKRYMENIVQEAKQKGVTLLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSAADIICKAM
 IDLAARLKEERLQARLLQVHDELILEAPKEEIERLCQLVPEVMEQAVTLRVLKVDYHYGPTWYDAK

SEQ ID NO: 79
 EQDELLIKLELPLATILAEMEFTGVKVDTKRL_EQMGEELAEQLRAVEQRIYELAGQEFNINSPKQLGI
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSAAEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYF
 ESFPGVKRYMETIVQEAKQKGVTLLHRRRLPDITSRNPNVRSFAERMAMNTPIQGSAADIICKAM
 IDLAARLKEERLQARLLQVHDELILEAPKEEIMERLCQLVPEVMEQAVTLRVLKVDYHYGPTWYDAK

SEQ ID NO: 80
 EQDELLTELEQPLALILAEMEFTGVKVDTKRL_EQMGEELAEQLKAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSAAEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEEVTANMRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYF
 ASFPGVKRYMEDIIVQEAKQKGVTLLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSAADIICKAM
 IDLAARLKEERLQARLLQVHDELILEAPKEEIERLCKLVPEVMEQAVELRVLKVDYHYGPTWYDAK

SEQ ID NO: 81
 EQYELFTDLEmplALILADMETYGVKVDVERLKEGMEEAERLKEIEQKIYELAGEEFNINSPKQLGV
 ILFEKLQLPVIKKKTGTGYSTSADVLEKLASKHEIIRNILHYRQLGKLQSTYIEGLLKVVHDTGKVHT
 MFNQALTQTGRLLSSTDPNLQNIPIRLEEGRKIRQAFVPSEEGWVIFAADYSQIELRVLAHIANDEKLI
 EAFRHMDIHTKTAMDVFHVSEDEVTSNMRQAKAVNFGIVYGISDYGLSQNLGITRKEAAEFIERYL
 ESFPGVKEYMDIVQEAKQKGVTLLHRRRLPEITSRNPNLRSFAERTAMNTPIQGSAADIICKAM
 IDMANRLKEENLQARLLQVHDELILEAPKEEIEKLKKIVPEVMEHAVELKVLKVDYSYGPWTWYDAK

SEQ ID NO: 82
 EQDELLTELEQPLAAILAEMEFTGVKVDTKRL_EQMGEELAEQLKEVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKKTGTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTKKVHT
 MFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFRDLDIHTKTAMDIFHVSEDEVNTANMRQAKAVNFGIVYGISDYGLSQNLNITRKEAAEFIERYF
 ESFPGVKRYMENIVQEAKQKGVTLLHRRRLPDITSRNPNVRSFAERTAMNTPIQGSAADIICKAM
 IDLAKRLKEERLQARLLQVHDELILEAPKEEIERLEKLVPEVMEQAVELRVLKVDYHYGPTWYDAK

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SEQ ID NO: 83
 EQDRLLTELEQPLASILAEMEFTGVKVDTKRLEQMGEELTEQLRAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKTKTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFFRRDLDIHTKTAMDIFHVSEEVTANMRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYF
 ASFPGVKQYMEMENIVQEAQKQGYTLLHRRRYLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELIILEAPKEEIERLCRLVPEVMEQAVTLRVLKVDYHYGPTWYDAK

SEQ ID NO: 84
 EQDRLLTELEQPLASILAEMEFTGVKVDTKRLEQMGEELAEQQLRAVEQRIYELAGQEFNINSPKQLGV
 ILFEKLQLPVLKTKTGYSTSADVLEKLAPHHEIVENILHYRQLGKLQSTYIEGLLKVVHPDTGKVHT
 MFNQALTQTGRLLSSTEPNLQNIPIRLEEGRKIRQAFVPSEPDWLIFAADYSQIELRVLAHIADDNL
 EAFFRRDLDIHTKTAMDIFHVSEEVTANMRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFIERYF
 ASFPGVKQYMEMENIVQEAQKQGYTLLHRRRYLPDITSRNFNVRSAERTAMNTPIQGSAADIIKKAM
 IDLAARLKEERLQARLLQVHDELIILEAPKEEIERLCRLVPEVMEQAVTLRVLKVDYHYGPTWYDAK

SEQ ID NO: 85
 EEEEKPLEDIEFAIADEITEEMLADKAALVVEVMEENYHDAPIVGIANVNEHGRFFLRPETALASPQF
 KAWLADETKKSMFDAKRAIVALWKKGIELRGVAFDLLAAYLLNPAQTAEDIAAVAKMKQYEAVRSD
 EAVYGKGKVKRSRSLPDEQALAEHLVRKAAAIWALEQPFMDDLRRK

SEQ ID NO: 86
 AEEEKPLEEMEFTDVDEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 VAWLEDETKKSMFDAKRAIVALWKKGIELRGVAFDLLAAYLLNPAQDDDVAAVAKMKQYEAVRSD
 EAVYGKGAKRSLPDEPTLAEHLVRKAAAIRALEQPFIDELRR

SEQ ID NO: 87
 EEEEKPLAEMEFTIADDEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNERGRFFLRPETALADPQF
 KAWLADETKKSMFDAKRAIVALWKKGIELRGVDFDLLAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYGKGAKRALPDEPTLAEHLVRKAAAIWALEEPFLDELREN

SEQ ID NO: 88
 AEEEKPLADMEFAIADEVTEEMLADKAALVVEVMEENYHDAPIVGFANVNEHGRFFLRRAELALADSQF
 LAWLADETKKSMFDKRAVALWKKGIELRGVAFDLLAAYLLNPAQDADDVAAVAKMKQYEAVRPD
 EAVYGKGAKRSLPDEPVLAEHLVRKAAAIWALERPFLDELRRN

SEQ ID NO: 89
 AEGEKPLAEMEFAIVDEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 LAWLADETKKSMFDKRAVALWKKGIELRGVAFDLLAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYGKGAKRSLPDEPTLAEHLVRKAAAIWALEQPFIDELRRN

SEQ ID NO: 90
 AEEEKPLEDIEFDIADEVTEEMLADKAALVVEVQEDNYHDAPIVGFAIVNEHGRFFIRTELADPQF
 KAWLADETKKSVFDAKRAIVALWKKGIELRGVDFDLLAAYLLNPAQTADDVAAVAKMKQYHAVRSD
 EAVYGKGAKRVPDEPVLAEHLVRKAAAIWALEEPFLDELRRN

SEQ ID NO: 91
 EEEEKPLEDISFEIADEVTEDMLTDESALVVEVLEENYHKADIVGFAIANENGNNFFIPTDTALASPQF
 KKWLEDETKKSVFDAKRAIVALWKHGIELKGVDFDLLIASYLLNPSESSDDFASVAKTKGYNAVQSD
 EAVYGKGAKRVPDEEKLAEHLARKAAIASALKETFIHELKEN

SEQ ID NO: 92
 TEEKELEDINVKTADEVTSMLTDPSALVVEQLGDNYHEADIIGFAIVNENGAFFIPKETALQSPQF
 KEWVEDETKKWVFDSDKRAIVALRWHGIELKGVDFDVLLASYIINPSNSYDDVASVKEYGLNIVSSD

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 EAVYKGAKRAVPAEDELAEHLGRKAAAISALRDKLLQALEEN

SEQ ID NO: 93
 AEEEVPLAEMEFVIADEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF

LAWLADETKKSMFDAKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD

EAVYKGAKRSLPDEPTLAEHLVRKAAAIAWALERPFLDELRRN

SEQ ID NO: 94
 AEEEKPLAEMEFVIADEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALASQF

VAWLADETKKSMFDAKRAIVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD

EAVYKGAKRAVDPDETLAEHLVRKAAAIAWALERPFLDELRRN

SEQ ID NO: 95
 EEEEVPLEEIIFAIADEVTEEMLADKAALVVEVLEENYHDAPIVGIALVNEHGRFFIRPETALASSQF

KAWLEDETKKSMFDAKRAIVALWKGIELRGVDFDLLLAAAYLLNPAQSAEDDVAAVAKMKQYEAVRSD

EAVYKGAKRAVDPDEPVLAEHLVRKAAAIAWALEEPFIDELREN

SEQ ID NO: 96
 AEEEAPLEDIEFDIADEVTEEMLADKAALVVEVQEDNYHDAPIVGFAIVNERGRFFIRTELASEAF

KAWLADETKKSMFDAKRAIVALWKGIELRGVDFDLLLAAAYLLNPAQTADDVAAVAKMKQYHAVRSD

EAVYKGAKRAVDPDEPVLAEHLVRKAAAIAWALEEPFIDELRKN

SEQ ID NO: 97
 AEEEKPLAEMEFIADEVTEEMLADKAALVVEVVEENYHDAPIVGIALVNEHGRFFLRPETALASQF

LAWLGDETKKSMFDKRAIVALWKGIELRGVAFDLLLAAAYLLNPAQQAAGDVAAVAKMKQYEAVRSD

EAVYKGAKRSVPDEPTLAEHLVRKAAAIAWALEQPFMDELRRN

SEQ ID NO: 98
 AEEEKPLAEMEFVIADEITDEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALASQF

VAWLADETKKSMFDAKRAIVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRPD

EAVYKGAKRSLPDEPTLAEHLVRKAAAIAWALERPFLDELRRN

SEQ ID NO: 99
 AEEEKPLEEMEFIADEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALASQF

KAWLADETKKSMFDAKRAIVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD

EAVYKGAKRAVDPDETLAEHLVRKAAAIAWALERPFLDELRRN

SEQ ID NO: 100
 AEEEVPLEEMEFTIADEITEEMLADKAALVVEVLEENYHDAPIVGIALVNEHGRFFLRPETALADPQF

VAWLADETKKSMFDAKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD

EAVYKGAKRSLPDEPVLAEHLVRKAAAIAWALERPFLDELREN

SEQ ID NO: 101
 AEEEVPLEEMEFVIADEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF

VAWLADETKKSMFDAKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD

EAVYKGAKRSLPDEPTLAEHLVRKAAAIAWALERPFLDELREN

SEQ ID NO: 102
 AEEEKPLAEMEFVIADGITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF

VAWLADETKKSMFDAKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD

EAVYKGAKRAVDPDETLAEHLVRKAAAIAWALERPFLDELRRN

SEQ ID NO: 103
 AEEEKPLEEMEFIADEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFMRPETALASQF

LAWLADETKKSMFDAKRAIVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDIAAVAKMKQYEAVRSD

EAVYKGKGVRSVPDEQLAEHLVRKAAAIAWALEQPFMDDLRRN

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SEQ ID NO: 104
 EEEEKPLEDISFEIADEVTEEMLTDESALVVEEVENYHKADIVGFAIVNENGNNFIPTDTALASPQF

KKWLEDETKKKTVFDAKRAIVALWKGIELKGVDFDLLIASYLLNPSETNDDFASVAKTKGYNAVQSD
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELRRN

SEQ ID NO: 105
 AEEEKPLAEMEFIADEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADSQF
 LAWLADETKKKSMFDAKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELRRN

SEQ ID NO: 106
 EEEEKPLAKIAFTLADRVTDEMLADKAALVVEVVEDNYHDAPIVGIAVVNEHGRFFLRPETALADPQF
 VAWLGDETKKKSVFDSKRAAVALWKGIELCGVSFDLLLAAAYLLDPAQGVDDVAAAAMKQYHAVRPD
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELRRN

SEQ ID NO: 107
 AEDEKPLEEIEFAIADEITEEMLADKAALVVEEVENYHDAPIVGFAIVNEHGRFFIRPETALASSQF
 KAWLADETKKKSMFDAKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQSAGDVAAVAKMKQYEAVRSD
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELREN

SEQ ID NO: 108
 AEEEAPLEDIEFDIADEVTEEMLADKAALVVEVQEDNYHDAPIVGFAIVNEHGRFFIRPETALASEAF
 KAWLADETKKKSVFDSKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQTADDVAAVAKMKQYHAVRSD
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELREN

SEQ ID NO: 109
 AEDEKPLAEMEFVIADGITDEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
 VAWLADETKKKSMFDAKRAAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELRRN

SEQ ID NO: 110
 TEEEVELEDINVKTTEVTSEMLTDPSALVVEQLGDNYHEADIIGFAIVNENGAFFIPKETALQSEAF
 KEWEDETKKKVFDSKRAAVALWKGIELKGVDFDVLASYIINPSNSYDDVASVKEYGLNIVSSD
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELREN

SEQ ID NO: 111
 AEKELPLMEMEFADADTTMEMLADKAALVVEVMEENYHDAPIVGIANVNEHGRFFLRTELALADPQF
 VAWLADETKKKSMFDAKRAAVALWKGIELVGVDFDLLLAAAYLLAPAQDDGAAAKAKMKQYEAVRED
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELREN

SEQ ID NO: 112
 AEDETPLMEMEFVIADGITDEMLADKAALVVEVQEENYHDAPIVGIALVNEHGRFFLRRAEMALADPQF
 VAWLADETKKKSMFDAKRAAVALWKGIELRGVDFDLLLAAAYLLNPAQTDEDVAAVAKMKQYEAVRSD
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELRSN

SEQ ID NO: 113
 AEEEKPLEDISFEIADEVTEEMLADEAALVVEEVENYHDAPIVGALVNEHGRFFIRPETALASSQF
 KAWLADETKKKSVFDSKRAAVALWKGIELRGVDFDLLLAAAYLLNPAQSAGDVAAVAKMKQYEAVRSD
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELREN

SEQ ID NO: 114
 SEEKPLAKMAFTLADEVTEEMLADKAALVVEVVEENYHDAPIVGIAVVNEHGRFFLRPETALASQF
 VAWLGDETKKKSMFDAKRAAVALWKGIELCGVSFDLLLAAAYLLDPAQGVDDVAAAAMKQYHAVRPD
 EAVYGKGAKRASPDEPLAEHLVRKAAAIWALERPFLDELRRN

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SEQ ID NO: 115
AEGEKPLAEMEFAIVDEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
LAWLADETKKKSMFDAKRAIVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
EAVYGKGAKRSLPDEPTLAEHLVRKAAAIWALEQPFIDELRRN

SEQ ID NO: 116
AEEEKPLAEMEFTIADVEVTEEMLADKAALVVEVLEENYHDAPIVGIALVNEHGRFFLRPETALADSQF
LAWLEDETKKKSMFDAKRAVALWKGIELRGVAFDLLLAAAYLLNPAQAGDVAAVAKMKQYEAVRSD
EAVYGKGAKRVPDEPVLAEHLVRKAAAIWALEEPFIDELRRN

SEQ ID NO: 117
AEEEKPLEEMEFAIADEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALASPQF
KAWLADETKKKSMFDAKRAIVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
EAVYGKGAKRVPDEPVLAEHLVRKAAAIWALERPFLDELRRN

SEQ ID NO: 118
AEEEKPLAEMEFAIADSVTEEMLADKAALVVEVVEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
LAWLGDETKKKSMFDKRAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
EAVYGKGAKRSPDEPTLAEHLVRKAAAIWALEQPFMDELRRN

SEQ ID NO: 119
AEEEKPLAEMEFAIADEITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
KAWLADETKKKSMFDAKRAIVALWKGIELRGVDFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
EAVYGKGAKRALPDEPTLAEHLVRKAAAIWALEEPFLDELREN

SEQ ID NO: 120
SEEKPLAKIAFDLADRVTTEEMLADKAALVVEVQEDNYHDAPIVGIAVVNEHGRFFLRAELALASPQF
VAWLGDETKKKSMFDKRAVALWKGIELCGVDFDLLLAAAYLLDPQTDDAAKAKMKQYHAVRPD
EAVYGKGAKRVPDEPVLAEHLVRKAAAIWALEEPFLDELRRN

SEQ ID NO: 121
AEDEKPLAEMEFAIADGITEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
LAWLADETKKKSMFDAKRAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
EAVYGKGAKRSLPDEPTLAEHLVRKAAAIWALEQPFMDELRSN

SEQ ID NO: 122
AEEEKPLEEMEFAIADEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
LAWLADETKKKSMFDAKRAVALWKGIELRGVAFDLLLAAAYLLNPAQDAGDVAAVAKMKQYEAVRSD
EAVYGKGAKRVPDEPVLAEHLVRKAAAIWALERPFLDELRRN

SEQ ID NO: 123
EEEEEPLEDISFEIVEEVTEDMLTDESALVVEVLEENYHKADIVGFAIANENGNFFIPTDTALASEAF
KKWLEDETKKKSVFDAKRAIVALWKHIELKGVDFDLLIASYLLNPSESSDDFASVAKTKGYNAVQSD
EAVYGKGAKRVPDEEKLAEHLARKAAAISALKETFIHELKEN

SEQ ID NO: 124
EEEEEPLEDISFEIVEEVTEEMLTDESALVVEVLEENYHKADIVGFAIVNENGNFFIPTDTALASEAF
KKWLEDETKKKTVFDAKRAIVALWKGIELKGVDFDLLIASYLLNPSETNDDFASVAKTKGYNAVQSD
EAVYGKGAKRVPPEEKLAEHLARKAAAISALKETFIQELKEN

SEQ ID NO: 125
AEEEKPLEEMEFAIADEVTEEMLADKAALVVEVMEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
KAWLADETKKKSMFDAKRAIVALWKGIELRGVAFDLLLAAAYLLNPAQDADDVAAVAKMKQYEAVRSD
EAVYGKGAKRVPDEPVLAEHLVRKAAAIRALERPFLDELRRN

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SEQ ID NO: 126
AEEEKPLAEMEFAIADSVTEEMLADKAALVVEENYHDAPIVGIALVNEHGRFFLRPETALADPQF
LAWLGETKKSMFDSKRAAVALKWKGIELRGVAFDLLLAAAYLLNPAQAAGDVAAVAKMKQEAVRSD
EAVYGKGAKRSVPDEPTLAEHLVRKAAAIWALEQPFMDELRRN

SEQ ID NO: 127
CAGCCAGCCGACGCCAGTTCGCTCATAGGAGATATGGTAGAGCCGC

SEQ ID NO: 128
GAGAGAATTGTACCACCTCCCACCGGGCACATAGCAGTCCTAGGGACAGT

SEQ ID NO: 129
GGCTTGGCTCTGCTAACACGTT

SEQ ID NO: 130
GGACGTTGTAATGTCCGCTCC

SEQ ID NO: 131
CTGCATAACGACGTGTCT

SEQ ID NO: 132
ACCATCTATGACTGTACGCC

SEQ ID NO: 133
CGCCAGGGTTTCCCAGTCACGAC

SEQ ID NO: 134
AGAACGGGAAGCTTGTCACTC

SEQ ID NO: 135
CGAACATGGGGCATCAG

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 135

<210> SEQ ID NO 1
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 1

Glu	Glu	Glu	Glu	Lys	Pro	Leu	Glu	Asp	Ile	Glu	Phe	Ala	Ile	Ala	Asp
1															
							5		10				15		

Glu	Ile	Thr	Glu	Glu	Met	Leu	Ala	Asp	Lys	Ala	Ala	Leu	Val	Val	Glu
							20		25			30			

Val	Met	Glu	Glu	Asn	Tyr	His	Asp	Ala	Pro	Ile	Val	Gly	Ile	Ala	Asn
							35		40		45				

Val	Asn	Glu	His	Gly	Arg	Phe	Phe	Leu	Arg	Pro	Glu	Thr	Ala	Leu	Ala
							50		55		60				

Ser	Pro	Gln	Phe	Lys	Ala	Trp	Leu	Ala	Asp	Glu	Thr	Lys	Lys	Ser
							65		70		75		80	

Met	Phe	Asp	Ala	Lys	Arg	Ala	Ile	Val	Ala	Leu	Lys	Trp	Lys	Gly	Ile
							85		90		95				

Glu	Leu	Arg	Gly	Val	Ala	Phe	Asp	Leu	Leu	Ala	Ala	Tyr	Leu	Leu
							100		105		110			

Asn	Pro	Ala	Gln	Thr	Ala	Glu	Asp	Ile	Ala	Ala	Val	Ala	Lys	Met	Lys
							115		120		125				

Gln	Tyr	Glu	Ala	Val	Arg	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Val
							130		135		140				

Lys	Arg	Ser	Leu	Pro	Asp	Glu	Gln	Ala	Leu	Ala	Glu	His	Leu	Val	Arg
							145		150		155		160		

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Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Asp Leu
165 170 175

Arg Lys Asn Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu
180 185 190

Ala Ser Ile Leu Ala Glu Met Glu Phe Thr Gly Val Asn Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Lys Glu
210 215 220

Gln Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu
370 375 380

Ala Phe Gln Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Glu Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Gln Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
565 570 575

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Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 2
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 2

Ala Glu Glu Glu Lys Pro Leu Glu Glu Met Glu Phe Thr Asp Val Asp
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Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Gln Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Val Ala Trp Leu Asp Glu Thr Lys Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Asp Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Arg Ala Leu Glu Gln Pro Phe Ile Asp Glu Leu
165 170 175

Arg Arg Arg Glu Gln Asp Glu Leu Phe Thr Lys Leu Glu Gln Pro Leu
180 185 190

Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Lys Glu
210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

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Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Glu Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Lys Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Glu Gln Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Arg Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 3
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 3

Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Thr Ile Ala Asp
1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu Arg Gly Arg Phe Phe Leu Arg Thr Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

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Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Leu Asp Glu Leu
165 170 175

Arg Glu Asn Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu
180 185 190

Ala Leu Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu
210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Pro His Arg Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Gln Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asp Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro

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545	550	555	560
Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp			
565	570	575	
Tyr Arg Tyr Gly Pro Thr Trp Tyr Asp Ala Lys			
580	585		

<210> SEQ ID NO 4
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 4

Ala Glu Glu Glu Lys Pro Leu Glu Asp Ile Glu Phe Asp Ile Ala Asp			
1	5	10	15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu			
20	25	30	

Val Gln Glu Asp Asn Tyr His Asp Ala Pro Ile Val Gly Phe Ala Ile			
35	40	45	

Val Asn Glu His Gly Arg Phe Phe Ile Arg Thr Glu Thr Ala Leu Ala			
50	55	60	

Ser Pro Gln Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser			
65	70	75	80

Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile			
85	90	95	

Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu			
100	105	110	

Asn Pro Ala Gln Thr Ala Asp Asp Val Ala Ala Val Ala Lys Met Lys			
115	120	125	

Gln Tyr His Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala			
130	135	140	

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg			
145	150	155	160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Leu Asp Glu Leu			
165	170	175	

Arg Lys Asn Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Leu Pro Leu			
180	185	190	

Ala Leu Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr			
195	200	205	

Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu			
210	215	220	

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn			
225	230	235	240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro			
245	250	255	

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu			
260	265	270	

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr			
275	280	285	

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys			
290	295	300	

Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala			
305	310	315	320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn			
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325	330	335
Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val		
340	345	350
Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile		
355	360	365
Glu Leu Arg Val Leu Ala His Ile Ala Asn Asp Asp Asn Leu Ile Glu		
370	375	380
Ala Phe Arg Arg Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val		
385	390	395
Phe His Val Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala		
405	410	415
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu		
420	425	430
Ser Gln Asn Leu Gly Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu		
435	440	445
Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Glu Tyr Met Glu Asp Ile		
450	455	460
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg		
465	470	475
Arg Arg Tyr Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser		
485	490	495
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala		
500	505	510
Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Ala Arg Leu Lys Glu		
515	520	525
Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile		
530	535	540
Phe Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro		
545	550	555
Glu Val Met Glu His Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp		
565	570	575
Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys		
580	585	

<210> SEQ ID NO 5
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 5

Thr Glu Glu Val Glu Leu Glu Asp Ile Asn Val Lys Thr Val Thr		
1	5	10
15		
Glu Val Thr Ser Glu Met Leu Thr Asp Pro Ser Ala Leu Val Val Glu		
20	25	30
Gln Leu Gly Asp Asn Tyr His Glu Ala Asp Ile Ile Gly Phe Ala Ile		
35	40	45
Val Asn Glu Asn Gly Ala Phe Phe Ile Pro Lys Glu Thr Ala Leu Gln		
50	55	60
Ser Glu Ala Phe Lys Glu Trp Val Glu Asp Glu Thr Lys Lys Lys Trp		
65	70	75
80		
Val Phe Asp Ser Lys Arg Ala Val Val Ala Leu Arg Trp His Gly Ile		
85	90	95
Glu Leu Lys Gly Val Asp Phe Asp Val Leu Leu Ala Ser Tyr Ile Ile		

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100	105	110
Asn Pro Ser Asn Ser Tyr Asp Asp Val Ala Ser Val Ala Lys Glu Tyr		
115	120	125
Gly Leu Asn Ile Val Ser Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala		
130	135	140
Lys Arg Ala Val Pro Ala Glu Asp Glu Leu Ala Glu His Leu Gly Arg		
145	150	155
Lys Ala Ala Ala Ile Ser Ala Leu Arg Asp Lys Leu Leu Gln Ala Leu		
165	170	175
Glu Glu Asn Asp Gln Tyr Glu Leu Phe Glu Asp Leu Glu Met Pro Leu		
180	185	190
Ala Leu Ile Leu Gly Glu Met Glu Ser Thr Gly Val Lys Val Asp Val		
195	200	205
Glu Arg Leu Lys Arg Met Gly Glu Glu Leu Thr Glu Lys Leu Lys Glu		
210	215	220
Tyr Glu Glu Lys Ile His Glu Leu Ala Gly Glu Pro Phe Asn Ile Asn		
225	230	235
Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gly Leu Pro		
245	250	255
Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu		
260	265	270
Glu Lys Leu Ala Asp Lys His Glu Ile Ile Arg Tyr Ile Leu His Tyr		
275	280	285
Arg Gln Ile Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys		
290	295	300
Val Thr Arg Lys Asp Thr His Lys Val His Thr Arg Phe Asn Gln Ala		
305	310	315
Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn		
325	330	335
Ile Pro Ile Arg Leu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val		
340	345	350
Pro Ser Glu Glu Gly Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile		
355	360	365
Glu Leu Arg Val Leu Ala His Ile Ser Lys Asp Glu Asn Leu Ile Glu		
370	375	380
Ala Phe Thr His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val		
385	390	395
Phe His Val Ser Glu Asp Glu Val Thr Ser Ala Met Arg Arg Gln Ala		
405	410	415
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu		
420	425	430
Ser Gln Asn Leu Gly Ile Thr Arg Lys Glu Ala Gly Ala Phe Ile Glu		
435	440	445
Arg Tyr Leu Glu Ser Phe Pro Gly Val Lys Ala Tyr Met Glu Asp Ile		
450	455	460
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg		
465	470	475
Arg Arg Tyr Ile Pro Glu Ile Thr Ser Arg Asn Phe Asn Ile Arg Ser		
485	490	495
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala		
500	505	510
Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Ala Arg Leu Lys Glu		
515	520	525

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Glu Asn Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Phe Glu Ala Pro Lys Glu Glu Ile Glu Ile Leu Glu Lys Ile Val Pro
545 550 555 560

Glu Val Met Glu His Ala Leu Glu Leu Asp Val Pro Leu Lys Val Asp
565 570 575

Tyr Ala Ser Gly Pro Ser Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 6

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 6

Glu Glu Glu Val Pro Leu Glu Glu Ile Glu Phe Ala Ile Ala Asp
1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Leu Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Phe Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Ile Arg Pro Glu Thr Ala Leu Ala
50 55 60

Ser Ser Gln Phe Lys Ala Trp Leu Glu Asp Glu Thr Lys Lys Lys Ser
65 70 75 80

Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Ser Ala Glu Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Ile Asp Glu Leu
165 170 175

Arg Glu Asn Glu Gln Asp Glu Leu Phe Thr Asp Leu Glu Gln Pro Leu
180 185 190

Ala Leu Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu
210 215 220

Ile Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

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Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Glu Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ser Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro
545 550 555 560

Glu Val Met Glu Asn Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ_ID NO 7

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 7

Ala Glu Glu Glu Ala Pro Leu Glu Asp Ile Glu Phe Asp Ile Ala Asp
1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Gln Glu Asp Asn Tyr His Asp Ala Pro Ile Val Gly Phe Ala Ile
35 40 45

Val Asn Glu Arg Gly Arg Phe Phe Ile Arg Thr Glu Thr Ala Leu Ala
50 55 60

Ser Glu Ala Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

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Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95
 Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110
 Asn Pro Ala Gln Thr Ala Asp Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125
 Gln Tyr His Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140
 Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
 145 150 155 160
 Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Leu Asp Glu Leu
 165 170 175
 Arg Lys Asn Glu Gln Asp Glu Leu Phe Thr Glu Leu Glu Leu Pro Leu
 180 185 190
 Ala Leu Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
 195 200 205
 Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu
 210 215 220
 Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240
 Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255
 Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270
 Glu Lys Leu Ala Pro His Arg Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285
 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asn Asp Asp Asn Leu Ile Glu
 370 375 380
 Ala Phe Arg Arg Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val
 385 390 395 400
 Phe His Val Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ser Gln Asn Leu Gly Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Gln Ser Phe Pro Gly Val Lys Glu Tyr Met Glu Asp Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480
 Arg Arg Phe Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser
 485 490 495

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Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Phe Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Glu Lys Leu Val Pro
545 550 555 560

Glu Val Met Glu His Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr Arg Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ_ID NO 8

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 8

Ala Glu Glu Glu Lys Pro Leu Glu Glu Met Glu Phe Ala Ile Ala Asp
1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Asp Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Arg Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Asn Asn Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu
180 185 190

Ala Ala Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu
210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

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Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285
 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val His Pro Asp Thr Lys Lys Val His Thr Arg Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
 370 375 380
 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400
 Phe His Val Ser Glu Asp Glu Val Thr Ala Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ser Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480
 Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
 485 490 495
 Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510
 Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Lys Arg Leu Lys Glu
 515 520 525
 Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
 530 535 540
 Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Glu Lys Leu Val Pro
 545 550 555 560
 Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
 565 570 575
 Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
 580 585

<210> SEQ ID NO 9
 <211> LENGTH: 587
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct
 <400> SEQUENCE: 9

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp
 1 5 10 15
 Ser Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30
 Val Val Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

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Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Leu Ala Trp Leu Gly Asp Glu Thr Lys Lys Lys Ser
65 70 75 80

Met Phe Asp Ser Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Ala Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Glu Leu
165 170 175

Arg Arg Asn Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu
180 185 190

Ala Ser Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Thr Glu Gln Leu Arg Ala
210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg

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465	470	475	480
Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser			
485	490	495	
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala			
500	505	510	
Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu			
515	520	525	
Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile			
530	535	540	
Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Arg Leu Val Pro			
545	550	555	560
Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp			
565	570	575	
Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys			
580	585		

<210> SEQ ID NO 10

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 10

1	5	10	15
Ala Glu Asp Glu Thr Pro Leu Met Glu Met Glu Phe Val Ile Ala Asp			
20	25	30	
Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu			
35	40	45	
Val Gln Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu			
50	55	60	
Asp Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser			
65	70	75	80
Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile			
85	90	95	
Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu			
100	105	110	
Asn Pro Ala Gln Thr Asp Glu Asp Val Ala Ala Val Ala Lys Met Lys			
115	120	125	
Gln Tyr Glu Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala			
130	135	140	
Lys Arg Pro Leu Pro Asp Glu Pro Ala Leu Ala Glu His Leu Val Arg			
145	150	155	160
Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu			
165	170	175	
Arg Ser Asn Glu Gln Asp Glu Leu Ile Lys Leu Glu Leu Pro Leu			
180	185	190	
Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr			
195	200	205	
Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala			
210	215	220	
Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn			
225	230	235	240
Ser Pro Lys Gln Leu Gly Ile Ile Leu Phe Glu Lys Leu Gln Leu Pro			

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245	250	255
Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu		
260	265	270
Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr		
275	280	285
Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys		
290	295	300
Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala		
305	310	315
Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn		
325	330	335
Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val		
340	345	350
Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile		
355	360	365
Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu		
370	375	380
Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile		
385	390	395
Phe His Val Ser Glu Glu Glu Val Thr Ala Arg Met Arg Arg Gln Ala		
405	410	415
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu		
420	425	430
Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu		
435	440	445
Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Thr Ile		
450	455	460
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg		
465	470	475
Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser		
485	490	495
Phe Ala Glu Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala		
500	505	510
Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu		
515	520	525
Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile		
530	535	540
Leu Glu Ala Pro Lys Glu Glu Met Glu Arg Leu Cys Gln Leu Val Pro		
545	550	555
Glu Val Met Glu Gln Ala Val Ala Leu Arg Val Pro Leu Lys Val Asp		
565	570	575
Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys		
580	585	

<210> SEQ_ID NO 11

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 11

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Thr Ile Ala Asp		
1	5	10
		15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu

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20	25	30
Val Leu Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu		
35	40	45
Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala		
50	55	60
Asp Ser Gln Phe Leu Ala Trp Leu Glu Asp Glu Thr Lys Lys Ser		
65	70	75
Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile		
85	90	95
Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu		
100	105	110
Asn Pro Ala Gln Ala Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys		
115	120	125
Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala		
130	135	140
Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg		
145	150	155
Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Ile Asp Glu Leu		
165	170	175
Arg Arg Asn Glu Gln Asp Arg Leu Leu Thr Asp Leu Glu Gln Pro Leu		
180	185	190
Ser Ser Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr		
195	200	205
Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Arg Ala		
210	215	220
Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn		
225	230	235
Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro		
245	250	255
Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu		
260	265	270
Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr		
275	280	285
Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys		
290	295	300
Val Val His Pro Asp Thr Gly Lys Val His Thr Ile Phe Asn Gln Ala		
305	310	315
Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn		
325	330	335
Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val		
340	345	350
Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile		
355	360	365
Glu Leu Arg Val Leu Ala His Ile Ala Asn Asp Asp Asn Leu Ile Glu		
370	375	380
Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile		
385	390	395
Phe His Val Ser Glu Asp Glu Val Thr Ala Asn Met Arg Arg Gln Ala		
405	410	415
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu		
420	425	430
Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu		
435	440	445

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Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ_ID NO 12

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 12

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp
1 5 10 15

Ser Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Val Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Leu Ala Trp Leu Gly Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ser Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Glu Leu
165 170 175

Arg Arg Asn Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu
180 185 190

Ala Ser Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Arg Ala
210 215 220

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Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Arg Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 13

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 13

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Ser Glu Glu Glu Lys Pro Leu Ala Lys Met Ala Phe Thr Leu Ala Asp
 1 5 10 15
 Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30
 Val Val Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Val
 35 40 45
 Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60
 Ser Pro Gln Phe Val Ala Trp Leu Gly Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80
 Met Phe Asp Ser Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95
 Glu Leu Cys Gly Val Ser Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110
 Asp Pro Ala Gln Gly Val Asp Asp Val Ala Ala Ala Lys Met Lys
 115 120 125
 Gln Tyr Glu Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140
 Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
 145 150 155 160
 Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
 165 170 175
 Arg Arg Asn Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu
 180 185 190
 Ser Ser Ile Leu Ala Glu Met Glu Phe Ala Gly Val Lys Val Asp Thr
 195 200 205
 Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu
 210 215 220
 Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240
 Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255
 Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270
 Glu Lys Leu Ala Pro Tyr His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285
 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val His Pro Asp Thr Lys Lys Val His Thr Arg Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Ser Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Glu Asp Asp Asn Leu Met Glu
 370 375 380
 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400
 Phe Gln Val Ser Glu Asp Glu Val Thr Pro Asn Met Arg Arg Gln Ala
 405 410 415

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Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Ser Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Asn Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Met Glu Arg Leu Cys Lys Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Ser Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 14

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 14

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Val Ile Ala Asp
1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Ser Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Arg Asn Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu
180 185 190

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Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
 195 200 205
 Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu
 210 215 220
 Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240
 Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255
 Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270
 Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285
 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu
 370 375 380
 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400
 Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480
 Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
 485 490 495
 Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510
 Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
 515 520 525
 Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
 530 535 540
 Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro
 545 550 555 560
 Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
 565 570 575
 Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
 580 585

<210> SEQ_ID NO 15
 <211> LENGTH: 587
 <212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 15

Ala	Glu	Glu	Glu	Lys	Pro	Leu	Ala	Glu	Met	Glu	Phe	Val	Ile	Ala	Asp
1									5			10			15

Gly	Ile	Thr	Glu	Glu	Met	Leu	Ala	Asp	Lys	Ala	Ala	Leu	Val	Val	Glu
									20			25			30

Val	Met	Glu	Glu	Asn	Tyr	His	Asp	Ala	Pro	Ile	Val	Gly	Ile	Ala	Leu
									35			40			45

Val	Asn	Glu	His	Gly	Arg	Phe	Phe	Leu	Arg	Pro	Glu	Thr	Ala	Leu	Ala
									50			55			60

Asp	Pro	Gln	Phe	Val	Ala	Trp	Leu	Ala	Asp	Glu	Thr	Lys	Lys	Lys	Ser
									65			70			80

Met	Phe	Asp	Ala	Lys	Arg	Ala	Ala	Val	Ala	Leu	Lys	Trp	Lys	Gly	Ile
									85			90			95

Glu	Leu	Arg	Gly	Val	Ala	Phe	Asp	Leu	Leu	Leu	Ala	Tyr	Leu	Leu	
									100			105			110

Asn	Pro	Ala	Gln	Asp	Ala	Gly	Asp	Val	Ala	Ala	Val	Ala	Lys	Met	Lys
									115			120			125

Gln	Tyr	Glu	Ala	Val	Arg	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Ala
									130			135			140

Lys	Arg	Ala	Val	Pro	Asp	Glu	Pro	Thr	Leu	Ala	Glu	His	Leu	Val	Arg
									145			150			160

Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Arg	Pro	Phe	Leu	Asp	Glu	Leu
									165			170			175

Arg	Arg	Asn	Glu	Gln	Asp	Glu	Leu	Leu	Ile	Lys	Leu	Glu	Gln	Pro	Leu
									180			185			190

Ala	Thr	Ile	Leu	Ala	Glu	Met	Glu	Phe	Thr	Gly	Val	Lys	Val	Asp	Thr
									195			200			205

Lys	Arg	Leu	Glu	Gln	Met	Gly	Glu	Leu	Ala	Glu	Gln	Leu	Gly	Ala	
									210			215			220

Val	Glu	Gln	Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile	Asn
									225			230			240

Ser	Pro	Lys	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu	Pro
									245			250			255

Val	Leu	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val	Leu	
									260			265			270

Glu	Lys	Leu	Ala	Pro	His	His	Glu	Ile	Val	Glu	Asn	Ile	Leu	His	Tyr
									275			280			285

Arg	Gln	Leu	Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu	Gly	Leu	Leu	Lys
									290			295			300

Val	Val	His	Pro	Asp	Thr	Gly	Lys	Val	His	Thr	Met	Phe	Asn	Gln	Ala
									305			310			320

Leu	Thr	Gln	Thr	Gly	Arg	Leu	Ser	Ser	Thr	Glu	Pro	Asn	Leu	Gln	Asn
									325			330			335

Ile	Pro	Ile	Arg	Leu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	Val	
									340			345			350

Pro	Ser	Glu	Pro	Asp	Trp	Leu	Ile	Phe	Ala	Ala	Asp	Tyr	Ser	Gln	Ile
									355			360			365

Glu	Leu	Arg	Val	Leu	Ala	His	Ile	Ala	Asp	Asp	Asp	Asn	Leu	Ile	Glu
									370			375			380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile

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385	390	395	400
Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala			
405	410	415	
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu			
420	425	430	
Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu			
435	440	445	
Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile			
450	455	460	
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg			
465	470	475	480
Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser			
485	490	495	
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala			
500	505	510	
Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu			
515	520	525	
Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile			
530	535	540	
Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Arg Leu Val Pro			
545	550	555	560
Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp			
565	570	575	
Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys			
580	585		

<210> SEQ_ID NO 16

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 16

Glu Glu Glu Glu Lys Pro Leu Glu Asp Ile Ser Phe Glu Ile Ala Asp			
1	5	10	15
Glu Val Thr Glu Asp Met Leu Thr Asp Glu Ser Ala Leu Val Val Glu			
20	25	30	
Val Leu Glu Glu Asn Tyr His Lys Ala Asp Ile Val Gly Phe Ala Ile			
35	40	45	
Ala Asn Glu Asn Gly Asn Phe Phe Ile Pro Thr Asp Thr Ala Leu Ala			
50	55	60	
Ser Pro Gln Phe Lys Lys Trp Leu Glu Asp Glu Thr Lys Lys Ser			
65	70	75	80
Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp His Gly Ile			
85	90	95	
Glu Leu Lys Gly Val Asp Phe Asp Leu Leu Ile Ala Ser Tyr Leu Leu			
100	105	110	
Asn Pro Ser Glu Ser Ser Asp Asp Phe Ala Ser Val Ala Lys Thr Lys			
115	120	125	
Gly Tyr Asn Ala Val Gln Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala			
130	135	140	
Lys Arg Ala Val Pro Asp Glu Glu Lys Leu Ala Glu His Leu Ala Arg			
145	150	155	160
Lys Ala Ala Ala Ile Ser Ala Leu Lys Glu Thr Phe Ile His Glu Leu			

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165	170	175
Lys Glu Asn Glu Gln Tyr Glu Leu Leu Thr Glu Leu Glu Met Pro Leu		
180	185	190
Ala Leu Ile Leu Ala Asp Met Glu Tyr Thr Gly Val Lys Val Asp Val		
195	200	205
Glu Arg Leu Lys Glu Met Gly Glu Glu Leu Thr Glu Arg Leu Lys Glu		
210	215	220
Ile Glu Gln Lys Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn		
225	230	235
Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gly Leu Pro		
245	250	255
Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu		
260	265	270
Glu Lys Leu Ala Ser His His Glu Ile Ile Arg His Ile Leu His Tyr		
275	280	285
Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys		
290	295	300
Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala		
305	310	315
Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn		
325	330	335
Ile Pro Ile Arg Leu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val		
340	345	350
Pro Ser Glu Pro Gly Trp Val Ile Phe Ala Ala Asp Tyr Ser Gln Ile		
355	360	365
Glu Leu Arg Val Leu Ala His Ile Ala Asn Asp Glu Asn Leu Ile Glu		
370	375	380
Ala Phe Arg His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val		
385	390	395
Phe His Val Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala		
405	410	415
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu		
420	425	430
Ser Gln Asn Leu Gly Ile Thr Arg Lys Glu Ala Gly Glu Phe Ile Glu		
435	440	445
Arg Tyr Leu Glu Ser Phe Pro Gly Val Lys Glu Tyr Met Asp Asp Ile		
450	455	460
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg		
465	470	475
Arg Arg Tyr Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser		
485	490	495
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala		
500	505	510
Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Asp Arg Leu Lys Glu		
515	520	525
Glu Asn Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile		
530	535	540
Phe Glu Ala Pro Lys Glu Glu Ile Glu Lys Leu Cys Lys Leu Val Pro		
545	550	555
Glu Val Met Glu Asn Ala Val Glu Leu Lys Val Pro Leu Lys Val Asp		
565	570	575
Tyr Ser Tyr Gly Pro Thr Trp Tyr Asp Ala Lys		
580	585	

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<210> SEQ_ID NO 17
 <211> LENGTH: 587
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

 <400> SEQUENCE: 17

Ala	Glu	Asp	Glu	Lys	Pro	Leu	Glu	Glu	Ile	Glu	Phe	Ala	Ile	Ala	Asp
1					5			10				15			
Glu	Ile	Thr	Glu	Glu	Met	Leu	Ala	Asp	Lys	Ala	Ala	Leu	Val	Val	Glu
	20					25			30						
Val	Leu	Glu	Glu	Asn	Tyr	His	Asp	Ala	Pro	Ile	Val	Gly	Phe	Ala	Ile
	35					40				45					
Val	Asn	Glu	His	Gly	Arg	Phe	Phe	Ile	Arg	Pro	Glu	Thr	Ala	Leu	Ala
	50					55			60						
Ser	Ser	Gln	Phe	Lys	Ala	Trp	Leu	Glu	Asp	Glu	Thr	Lys	Lys	Ser	
65						70			75			80			
Met	Phe	Asp	Ala	Lys	Arg	Ala	Ala	Val	Ala	Leu	Lys	Trp	Lys	Gly	Ile
	85					90			95						
Glu	Leu	Arg	Gly	Val	Ala	Phe	Asp	Leu	Leu	Leu	Ala	Tyr	Leu	Leu	
	100					105			110						
Asn	Pro	Ala	Gln	Ser	Ala	Gly	Asp	Val	Ala	Ala	Val	Ala	Lys	Met	Lys
	115					120			125						
Gln	Tyr	Glu	Ala	Val	Arg	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Ala
	130					135			140						
Lys	Arg	Ala	Val	Pro	Asp	Glu	Pro	Thr	Leu	Ala	Glu	His	Leu	Val	Arg
145						150			155			160			
Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Gln	Pro	Phe	Leu	Asp	Glu	Leu
	165					170			175						
Arg	Glu	Asn	Glu	Gln	Asp	Glu	Leu	Leu	Thr	Lys	Leu	Glu	Gln	Pro	Leu
	180					185			190						
Ala	Leu	Ile	Leu	Ala	Glu	Met	Glu	Phe	Thr	Gly	Val	Lys	Val	Asp	Thr
	195					200			205						
Lys	Arg	Leu	Glu	Gln	Met	Gly	Glu	Glu	Leu	Ala	Glu	Gln	Leu	Lys	Glu
	210					215			220						
Ile	Glu	Gln	Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile	Asn
225						230			235			240			
Ser	Pro	Lys	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu	Pro
	245					250			255						
Val	Leu	Lys	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val	Leu
	260					265			270						
Glu	Lys	Leu	Ala	Pro	His	His	Glu	Ile	Val	Glu	Asn	Ile	Leu	His	Tyr
	275					280			285						
Arg	Gln	Leu	Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu	Gly	Leu	Leu	Lys
	290					295			300						
Val	Val	Arg	Pro	Asp	Thr	Gly	Lys	Val	His	Thr	Met	Phe	Asn	Gln	Ala
305						310			315			320			
Leu	Thr	Gln	Thr	Gly	Arg	Leu	Ser	Ser	Thr	Glu	Pro	Asn	Leu	Gln	Asn
	325					330			335						
Ile	Pro	Ile	Arg	Leu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	Val	
	340					345			350						
Pro	Ser	Glu	Pro	Asp	Trp	Leu	Ile	Phe	Ala	Ala	Asp	Tyr	Ser	Gln	Ile
	355					360			365						

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Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ser Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Glu Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 18
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 18

Ala Glu Glu Glu Lys Pro Leu Ala Asp Met Glu Phe Ala Ile Ala Asp
1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Asp Asn Tyr His Asp Ala Pro Ile Val Gly Phe Ala Asn
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Ala Glu Leu Ala Leu Ala
50 55 60

Asp Ser Gln Phe Leu Ala Trp Leu Glu Asp Glu Thr Lys Lys Lys Ser
65 70 75 80

Met Phe Asp Arg Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Asp Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

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Lys Arg Ser Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Arg Asn Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu
180 185 190

Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala
210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asn Asp Asp Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Val
385 390 395 400

Phe His Val Ser Glu Glu Val Thr Ala Arg Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro
545 550 555 560

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Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
 565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
 580 585

<210> SEQ ID NO 19
 <211> LENGTH: 587
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 19

Ala Glu Gly Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Val Asp
 1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60

Asp Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
 65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Ile Asp Glu Leu
 165 170 175

Arg Arg Asn Glu Gln Asp Glu Leu Leu Thr Lys Leu Glu Gln Pro Leu
 180 185 190

Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
 195 200 205

Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Gly Ala
 210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255

Val Leu Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
 305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
 325 330 335

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Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 20

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 20

Ala Glu Glu Lys Pro Leu Glu Glu Met Glu Phe Ala Ile Ala Asp
1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Met Arg Pro Glu Thr Ala Leu Ala
50 55 60

Ser Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Tyr Leu Leu
100 105 110

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Asn Pro Ala Gln Asp Ala Gly Asp Ile Ala Ala Val Ala Lys Met Lys
 115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Val
 130 135 140

Lys Arg Ser Leu Pro Asp Glu Gln Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Asp Leu
 165 170 175

Arg Asn Asn Glu Gln Asp Gln Leu Leu Thr Glu Leu Glu Gln Pro Leu
 180 185 190

Ala Ala Ile Leu Ala Glu Met Glu Phe Thr Gly Val Asn Val Asp Thr
 195 200 205

Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Lys Glu
 210 215 220

Ile Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
 305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
 325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
 370 375 380

Ala Phe Gln Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400

Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
 405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430

Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile
 450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
 485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
 515 520 525

Glu Gln Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile

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530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro
 545 550 555 560

Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
 565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
 580 585

<210> SEQ ID NO 21

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 21

Thr Glu Glu Glu Lys Glu Leu Glu Asp Ile Asn Val Lys Thr Ala Asp
 1 5 10 15

Glu Val Thr Ser Glu Met Leu Thr Asp Pro Ser Ala Leu Val Val Glu
 20 25 30

Gln Leu Gly Asp Asn Tyr His Glu Ala Asp Ile Ile Gly Phe Ala Ile
 35 40 45

Val Asn Glu Asn Gly Ala Phe Phe Ile Pro Lys Glu Thr Ala Leu Gln
 50 55 60

Ser Pro Gln Phe Lys Glu Trp Val Glu Asp Glu Thr Lys Lys Lys Trp
 65 70 75 80

Val Phe Asp Ser Lys Arg Ala Ile Val Ala Leu Arg Trp His Gly Ile
 85 90 95

Glu Leu Lys Gly Val Asp Phe Asp Val Leu Leu Ala Ser Tyr Ile Ile
 100 105 110

Asn Pro Ser Asn Ser Tyr Asp Asp Val Ala Ser Val Ala Lys Glu Tyr
 115 120 125

Gly Leu Asn Ile Val Ser Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

Lys Arg Ala Val Pro Ala Glu Asp Glu Leu Ala Glu His Leu Gly Arg
 145 150 155 160

Lys Ala Ala Ala Ile Ser Ala Leu Arg Asp Lys Leu Leu Gln Ala Leu
 165 170 175

Glu Glu Asn Asp Gln Tyr Glu Leu Leu Thr Glu Leu Glu Met Pro Leu
 180 185 190

Ala Leu Ile Leu Gly Glu Met Glu Ser Thr Gly Val Lys Val Asp Val
 195 200 205

Glu Arg Leu Lys Arg Met Gly Glu Glu Leu Thr Glu Lys Leu Lys Glu
 210 215 220

Tyr Glu Glu Lys Ile His Glu Leu Ala Gly Glu Pro Phe Asn Ile Asn
 225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gly Leu Pro
 245 250 255

Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270

Glu Lys Leu Ala Asp Lys His Glu Ile Ile Arg Tyr Ile Leu His Tyr
 275 280 285

Arg Gln Ile Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300

Val Thr Arg Lys Asp Thr His Lys Val His Thr Arg Phe Asn Gln Ala

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305	310	315	320
Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn			
325	330	335	
Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val			
340	345	350	
Pro Ser Glu Glu Gly Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile			
355	360	365	
Glu Leu Arg Val Leu Ala His Ile Ser Lys Asp Glu Asn Leu Ile Glu			
370	375	380	
Ala Phe Thr His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val			
385	390	395	400
Phe His Val Ser Glu Asp Glu Val Thr Ser Ala Met Arg Arg Gln Ala			
405	410	415	
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu			
420	425	430	
Ser Gln Asn Leu Gly Ile Thr Arg Lys Glu Ala Gly Ala Phe Ile Glu			
435	440	445	
Arg Tyr Leu Glu Ser Phe Pro Gly Val Lys Ala Tyr Met Glu Asp Ile			
450	455	460	
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg			
465	470	475	480
Arg Arg Tyr Ile Pro Glu Ile Thr Ser Arg Asn Phe Asn Ile Arg Ser			
485	490	495	
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala			
500	505	510	
Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Ala Arg Leu Lys Glu			
515	520	525	
Glu Asn Leu Gln Ala Arg Leu Leu Gln Val His Asp Glu Leu Ile			
530	535	540	
Phe Glu Ala Pro Lys Glu Glu Ile Glu Ile Leu Cys Lys Leu Val Pro			
545	550	555	560
Glu Val Met Glu His Ala Val Glu Leu Asp Val Pro Leu Lys Val Asp			
565	570	575	
Tyr Ala Ser Gly Pro Ser Trp Tyr Asp Ala Lys			
580	585		

<210> SEQ ID NO 22
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 22

Ala Glu Glu Glu Lys Pro Leu Glu Glu Met Glu Phe Ala Ile Ala Asp			
1	5	10	15
Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu			
20	25	30	
Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu			
35	40	45	
Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala			
50	55	60	
Ser Pro Gln Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser			
65	70	75	80
Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile			

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85	90	95
Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu		
100	105	110
Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys		
115	120	125
Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala		
130	135	140
Lys Arg Ala Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg		
145	150	155
160		
Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu		
165	170	175
Arg Asn Asn Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu		
180	185	190
Ala Leu Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr		
195	200	205
Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu		
210	215	220
Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn		
225	230	235
240		
Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro		
245	250	255
Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu		
260	265	270
Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr		
275	280	285
Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys		
290	295	300
Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala		
305	310	315
320		
Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn		
325	330	335
Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val		
340	345	350
Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile		
355	360	365
Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu		
370	375	380
Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile		
385	390	395
400		
Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala		
405	410	415
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu		
420	425	430
Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu		
435	440	445
Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile		
450	455	460
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg		
465	470	475
480		
Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser		
485	490	495
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala		
500	505	510

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Asp	Ile	Ile	Lys	Lys	Ala	Met	Ile	Asp	Leu	Ala	Ala	Arg	Leu	Lys	Glu
515															525
Glu	Arg	Leu	Gln	Ala	Arg	Leu	Leu	Leu	Gln	Val	His	Asp	Glu	Leu	Ile
530															540
Leu	Glu	Ala	Pro	Lys	Glu	Glu	Ile	Glu	Arg	Leu	Cys	Lys	Leu	Val	Pro
545															555
Glu	Val	Met	Glu	Gln	Ala	Val	Glu	Leu	Arg	Val	Pro	Leu	Lys	Val	Asp
565															575
Tyr	His	Tyr	Gly	Pro	Thr	Trp	Tyr	Asp	Ala	Lys					
580															585

<210> SEQ ID NO 23
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 23

Glu	Glu	Glu	Lys	Pro	Leu	Glu	Asp	Ile	Ser	Phe	Glu	Ile	Ala	Asp	
1								5		10				15	
Glu	Val	Thr	Glu	Glu	Met	Leu	Thr	Asp	Glu	Ser	Ala	Leu	Val	Val	Glu
								20		25				30	
Val	Leu	Glu	Glu	Asn	Tyr	His	Lys	Ala	Asp	Ile	Val	Gly	Phe	Ala	Ile
								35		40				45	
Val	Asn	Glu	Asn	Gly	Asn	Phe	Phe	Ile	Pro	Thr	Asp	Thr	Ala	Leu	Ala
								50		55				60	
Ser	Pro	Gln	Phe	Lys	Lys	Trp	Leu	Glu	Asp	Glu	Thr	Lys	Lys	Thr	
								65		70				80	
Val	Phe	Asp	Ala	Lys	Arg	Ala	Ile	Val	Ala	Leu	Lys	Trp	Lys	Gly	Ile
								85		90				95	
Glu	Leu	Lys	Gly	Val	Asp	Phe	Asp	Leu	Leu	Ile	Ala	Ser	Tyr	Leu	Leu
								100		105				110	
Asn	Pro	Ser	Glu	Thr	Asn	Asp	Asp	Phe	Ala	Ser	Val	Ala	Lys	Thr	Lys
								115		120				125	
Gly	Tyr	Asn	Ala	Val	Gln	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Ala
								130		135				140	
Lys	Arg	Ala	Val	Pro	Glu	Glu	Lys	Leu	Ala	Glu	His	Leu	Ala	Arg	
								145		150				160	
Lys	Ala	Ala	Ala	Ile	Ser	Ala	Leu	Lys	Glu	Thr	Phe	Ile	Gln	Glu	Leu
								165		170				175	
Lys	Glu	Asn	Glu	Gln	Tyr	Glu	Leu	Leu	Thr	Glu	Leu	Glu	Met	Pro	Leu
								180		185				190	
Ala	Leu	Ile	Leu	Ala	Asp	Met	Glu	Tyr	Thr	Gly	Val	Lys	Val	Asp	Val
								195		200				205	
Glu	Arg	Leu	Lys	Glu	Met	Gly	Glu	Leu	Ala	Glu	Arg	Leu	Lys	Glu	
								210		215				220	
Ile	Glu	Gln	Lys	Ile	Tyr	Glu	Leu	Ala	Gly	Glu	Glu	Phe	Asn	Ile	Asn
								225		230				240	
Ser	Pro	Lys	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gly	Leu	Pro
								245		250				255	
Val	Ile	Lys	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val	Leu
								260		265				270	
Glu	Lys	Leu	Ala	Ser	Lys	His	Glu	Ile	Ile	Arg	Asn	Ile	Leu	His	Tyr
								275		280				285	

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Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Glu Gly Trp Val Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asn Asp Glu Lys Leu Ile Glu
 370 375 380
 Ala Phe Arg His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val
 385 390 395 400
 Phe His Val Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ser Gln Asn Leu Gly Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Leu Glu Ser Phe Pro Gly Val Lys Glu Tyr Met Asp Asp Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480
 Arg Arg Tyr Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser
 485 490 495
 Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510
 Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Asn Arg Leu Lys Glu
 515 520 525
 Glu Asn Leu Gln Ala Arg Leu Leu Gln Val His Asp Glu Leu Ile
 530 535 540
 Phe Glu Ala Pro Lys Glu Glu Ile Glu Lys Cys Lys Lys Ile Val Pro
 545 550 555 560
 Glu Val Met Glu His Ala Val Glu Leu Lys Val Pro Leu Lys Val Asp
 565 570 575
 Tyr Ser Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
 580 585

<210> SEQ ID NO 24
 <211> LENGTH: 587
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 24

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp
 1 5 10 15
 Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30
 Val Val Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45
 Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60

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Ser Pro Gln Phe Leu Ala Trp Leu Gly Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80
 Met Phe Asp Ser Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95
 Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
 100 105 110
 Asn Pro Ala Gln Ala Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125
 Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140
 Lys Arg Ser Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160
 Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Glu Leu
 165 170 175
 Arg Arg Asn Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu
 180 185 190
 Ala Ser Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
 195 200 205
 Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Thr Glu Gln Leu Lys Glu
 210 215 220
 Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240
 Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255
 Val Leu Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270
 Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285
 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu
 370 375 380
 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400
 Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480

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Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 25

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 25

Ala Glu Glu Glu Val Pro Leu Glu Met Glu Phe Thr Ile Ala Asp
1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Leu Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Val Ala Trp Leu Glu Asp Glu Thr Lys Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Glu Asn Glu Gln Asp Glu Leu Leu Thr Asp Leu Glu Gln Pro Leu
180 185 190

Ser Ser Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Arg Ala
210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

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Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Ile Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 26

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 26

Ala Glu Glu Glu Ala Pro Leu Glu Asp Ile Glu Phe Asp Ile Ala Asp
1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

-continued

Val Gln Glu Asp Asn Tyr His Asp Ala Pro Ile Val Gly Phe Ala Ile
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Ile Arg Thr Glu Thr Ala Leu Ala
 50 55 60

Ser Glu Ala Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80

Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asn Pro Ala Gln Thr Ala Asp Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

Gln Tyr His Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Leu Asp Glu Leu
 165 170 175

Arg Lys Asn Glu Gln Asp Glu Leu Phe Thr Glu Leu Glu Leu Pro Leu
 180 185 190

Ala Leu Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
 195 200 205

Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu
 210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255

Val Leu Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
 305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn
 325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asn Asp Asp Asn Leu Ile Glu
 370 375 380

Ala Phe Arg Arg Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val
 385 390 395 400

Phe His Val Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala
 405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430

Ser Gln Asn Leu Gly Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445

Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Glu Tyr Met Glu Asp Ile

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450	455	460
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg		
465	470	475
Arg Arg Tyr Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser		
485	490	495
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala		
500	505	510
Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Ala Arg Leu Lys Glu		
515	520	525
Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile		
530	535	540
Phe Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Glu Lys Leu Val Pro		
545	550	555
Glu Val Met Glu His Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp		
565	570	575
Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys		
580	585	

<210> SEQ ID NO 27
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 27

Ala Glu Glu Glu Val Pro Leu Glu Glu Met Glu Phe Val Ile Ala Asp		
1	5	10
Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu		
20	25	30
Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu		
35	40	45
Val Asn Glu His Gly Arg Phe Phe Leu Arg Ala Glu Thr Ala Leu Ala		
50	55	60
Asp Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser		
65	70	75
Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile		
85	90	95
Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu		
100	105	110
Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys		
115	120	125
Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala		
130	135	140
Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg		
145	150	155
Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu		
165	170	175
Arg Glu Asn Glu Gln Asp Glu Leu Leu Ile Lys Leu Glu Gln Pro Leu		
180	185	190
Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr		
195	200	205
Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala		
210	215	220
Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn		

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225	230	235	240
Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro			
245	250	255	
Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu			
260	265	270	
Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr			
275	280	285	
Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys			
290	295	300	
Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala			
305	310	315	320
Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn			
325	330	335	
Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val			
340	345	350	
Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile			
355	360	365	
Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu			
370	375	380	
Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile			
385	390	395	400
Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala			
405	410	415	
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu			
420	425	430	
Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu			
435	440	445	
Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile			
450	455	460	
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg			
465	470	475	480
Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser			
485	490	495	
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala			
500	505	510	
Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu			
515	520	525	
Glu Arg Leu Gln Ala Arg Leu Leu Gln Val His Asp Glu Leu Ile			
530	535	540	
Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro			
545	550	555	560
Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp			
565	570	575	
Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys			
580	585		

<210> SEQ_ID NO 28

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 28

Glu Glu Glu Lys Pro Leu Ala Lys Ile Ala Phe Thr Leu Ala Asp

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1	5	10	15
Arg Val Thr Asp Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu			
20	25	30	
Val Val Glu Asp Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Val			
35	40	45	
Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala			
50	55	60	
Asp Pro Gln Phe Val Ala Trp Leu Gly Asp Glu Thr Lys Lys Lys Ser			
65	70	75	80
Val Phe Asp Ser Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile			
85	90	95	
Glu Leu Cys Gly Val Ser Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu			
100	105	110	
Asp Pro Ala Gln Gly Val Asp Asp Val Ala Ala Ala Lys Met Lys			
115	120	125	
Gln Tyr His Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala			
130	135	140	
Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg			
145	150	155	160
Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu			
165	170	175	
Arg Arg Asn Glu Gln Asp Arg Leu Leu Val Glu Leu Glu Gln Pro Leu			
180	185	190	
Ser Ser Ile Leu Ala Glu Met Glu Phe Ala Gly Val Lys Val Asp Thr			
195	200	205	
Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu			
210	215	220	
Gln Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn			
225	230	235	240
Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro			
245	250	255	
Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu			
260	265	270	
Glu Lys Leu Ala Pro Tyr His Glu Ile Val Glu Asn Ile Leu His Tyr			
275	280	285	
Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys			
290	295	300	
Val Val Arg Pro Asp Thr Lys Lys Val His Thr Ile Phe Asn Gln Ala			
305	310	315	320
Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn			
325	330	335	
Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val			
340	345	350	
Pro Ser Glu Ser Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile			
355	360	365	
Glu Leu Arg Val Leu Ala His Ile Ala Glu Asp Glu Asn Leu Met Glu			
370	375	380	
Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile			
385	390	395	400
Phe Gln Val Ser Glu Asp Glu Val Thr Pro Asn Met Arg Arg Gln Ala			
405	410	415	
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu			
420	425	430	

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Ser Gln Asn Leu Gly Ile Ser Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445

Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
 450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480

Arg Arg Tyr Asp Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
 485 490 495

Phe Ala Glu Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Asn Ala Arg Leu Lys Glu
 515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
 530 535 540

Leu Glu Ala Pro Lys Glu Glu Met Glu Arg Leu Cys Arg Leu Val Pro
 545 550 555 560

Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
 565 570 575

Tyr His Tyr Gly Ser Thr Trp Tyr Asp Ala Lys
 580 585

<210> SEQ ID NO 29
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 29

Ala Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp
 1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60

Asp Ser Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
 65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

Lys Arg Ser Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Leu Asp Glu Leu
 165 170 175

Arg Arg Asn Glu Gln Asp Arg Leu Leu Thr Lys Leu Glu Gln Pro Leu
 180 185 190

Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
 195 200 205

-continued

Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala
210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 30
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 30

Ala Glu Glu Glu Val Pro Leu Ala Glu Met Glu Phe Val Ile Ala Asp
 1 5 10 15

 Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

 Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

 Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60

 Asp Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
 65 70 75 80

 Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

 Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

 Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

 Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

 Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160

 Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
 165 170 175

 Arg Arg Asn Glu Gln Asp Glu Leu Leu Thr Lys Leu Glu Gln Pro Leu
 180 185 190

 Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
 195 200 205

 Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala
 210 215 220

 Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240

 Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255

 Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270

 Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285

 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300

 Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
 305 310 315 320

 Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
 325 330 335

 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350

 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365

 Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
 370 375 380

 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400

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Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 31
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 31

Ala Glu Asp Glu Lys Pro Leu Ala Glu Met Glu Phe Val Ile Ala Asp
1 5 10 15

Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

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Arg Arg Asn Glu Gln Asp Arg Leu Leu Ile Lys Leu Glu Gln Pro Leu
 180 185 190
 Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
 195 200 205
 Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala
 210 215 220
 Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240
 Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255
 Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270
 Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285
 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
 370 375 380
 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400
 Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480
 Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
 485 490 495
 Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510
 Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
 515 520 525
 Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
 530 535 540
 Leu Glu Ala Pro Lys Glu Glu Met Glu Arg Leu Cys Arg Leu Val Pro
 545 550 555 560
 Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
 565 570 575
 Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
 580 585

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<210> SEQ_ID NO 32
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 32

Glu Glu Glu Glu Pro Leu Glu Asp Ile Ser Phe Glu Ile Val Glu
1           5          10          15

Glu Val Thr Glu Glu Met Leu Thr Asp Glu Ser Ala Leu Val Val Glu
20          25          30

Val Leu Glu Glu Asn Tyr His Lys Ala Asp Ile Val Gly Phe Ala Ile
35          40          45

Val Asn Glu Asn Gly Asn Phe Phe Ile Pro Thr Asp Thr Ala Leu Ala
50          55          60

Ser Glu Ala Phe Lys Lys Trp Leu Glu Asp Glu Thr Lys Lys Lys Thr
65          70          75          80

Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85          90          95

Glu Leu Lys Gly Val Asp Phe Asp Leu Leu Ile Ala Ser Tyr Leu Leu
100         105         110

Asn Pro Ser Glu Thr Asn Asp Asp Phe Ala Ser Val Ala Lys Thr Lys
115         120         125

Gly Tyr Asn Ala Val Gln Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130         135         140

Lys Arg Ala Val Pro Glu Glu Glu Lys Leu Ala Glu His Leu Ala Arg
145         150         155         160

Lys Ala Ala Ala Ile Ser Ala Leu Lys Glu Thr Phe Ile Gln Glu Leu
165         170         175

Lys Glu Asn Glu Gln Tyr Glu Leu Phe Thr Asp Leu Glu Met Pro Leu
180         185         190

Ala Leu Ile Leu Ala Asp Met Glu Tyr Thr Gly Val Lys Val Asp Val
195         200         205

Glu Arg Leu Lys Glu Met Gly Glu Glu Leu Ala Glu Arg Leu Lys Glu
210         215         220

Ile Glu Gln Lys Ile Tyr Glu Leu Ala Gly Glu Glu Phe Asn Ile Asn
225         230         235         240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gly Leu Pro
245         250         255

Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260         265         270

Glu Lys Leu Ala Ser Lys His Glu Ile Ile Arg Asn Ile Leu His Tyr
275         280         285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290         295         300

Val Val His Gln Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
305         310         315         320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn
325         330         335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340         345         350

Pro Ser Glu Glu Gly Trp Val Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355         360         365

Glu Leu Arg Val Leu Ala His Ile Ala Asn Asp Glu Lys Leu Ile Glu

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370	375	380
Ala Phe Arg His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val		
385	390	395
Phe His Val Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala		
405	410	415
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu		
420	425	430
Ser Gln Asn Leu Gly Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu		
435	440	445
Arg Tyr Leu Glu Ser Phe Pro Gly Val Lys Glu Tyr Met Asp Asp Ile		
450	455	460
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg		
465	470	475
Arg Arg Tyr Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser		
485	490	495
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala		
500	505	510
Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Asn Arg Leu Lys Glu		
515	520	525
Glu Asn Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile		
530	535	540
Phe Glu Ala Pro Lys Glu Glu Ile Glu Lys Leu Lys Lys Ile Val Pro		
545	550	555
Glu Val Met Glu His Ala Val Glu Leu Lys Val Pro Leu Lys Val Asp		
565	570	575
Tyr Ser Tyr Gly Pro Thr Trp Tyr Asp Ala Lys		
580	585	

<210> SEQ ID NO 33

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 33

Ala Glu Lys Glu Leu Pro Leu Met Glu Met Glu Phe Ala Asp Ala Asp		
1	5	10
Thr Ile Thr Met Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu		
20	25	30
Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Asn		
35	40	45
Val Asn Glu His Gly Arg Phe Phe Leu Arg Thr Glu Leu Ala Leu Ala		
50	55	60
Asp Phe Gln Phe Val Ala Trp Leu Glu Asp Glu Thr Lys Lys Lys Ser		
65	70	75
Met Phe Asp Arg Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile		
85	90	95
Glu Leu Val Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu		
100	105	110
Ala Pro Ala Gln Asp Asp Gly Asp Ala Ala Ala Lys Ala Lys Met Lys		
115	120	125
Gln Tyr Glu Ala Val Arg Glu Asp Glu Ala Val Tyr Gly Lys Gly Ala		
130	135	140
Lys Arg Pro Asp Pro Asp Glu Leu Ala Leu Ala Glu His Leu Val Arg		

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145	150	155	160
Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu			
165	170	175	
Arg Glu Asn Glu Gln Asp Leu Leu Leu Glu Leu Glu Gln Pro Leu			
180	185	190	
Ile Leu Ile Leu Ala Glu Met Glu Phe Thr Gly Val Asp Val Asp Thr			
195	200	205	
Lys Arg Leu Glu Gln Met Gly Leu Glu Leu Ala Glu Gln Leu Val Glu			
210	215	220	
Gln Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn			
225	230	235	240
Ser Pro Lys Gln Leu Gly Leu Ile Leu Phe Glu Lys Leu Gln Leu Pro			
245	250	255	
Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu			
260	265	270	
Glu Lys Leu Ala Pro Glu His Glu Ile Val Glu Asn Ile Leu His Tyr			
275	280	285	
Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys			
290	295	300	
Val Val Asp Thr Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala			
305	310	315	320
Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn			
325	330	335	
Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val			
340	345	350	
Pro Ser Glu Pro Leu Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile			
355	360	365	
Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ala Glu			
370	375	380	
Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile			
385	390	395	400
Phe His Val Ser Glu Glu Val Thr Ala Arg Met Arg Arg Gln Ala			
405	410	415	
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu			
420	425	430	
Ala Gln Asn Leu Asn Ile Lys Arg Lys Glu Ala Ala Glu Phe Ile Glu			
435	440	445	
Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Val Ile			
450	455	460	
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg			
465	470	475	480
Arg Arg Tyr Asp Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser			
485	490	495	
Phe Ala Glu Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala			
500	505	510	
Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu			
515	520	525	
Glu Gln Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile			
530	535	540	
Leu Glu Ala Pro Lys Glu Glu Met Glu Arg Leu Cys Val Leu Val Pro			
545	550	555	560
Glu Val Met Glu Gln Ala Val Arg Leu Arg Val Pro Leu Lys Val Asp			
565	570	575	

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Tyr His Tyr Gly Trp Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 34
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 34

Ser	Glu	Glu	Glu	Lys	Pro	Leu	Ala	Lys	Ile	Ala	Phe	Asp	Leu	Ala	Asp
1									10						15
Arg	Val	Thr	Glu	Glu	Met	Leu	Ala	Asp	Lys	Ala	Ala	Leu	Val	Val	Glu
	20								25						30
Val	Gln	Glu	Asp	Asn	Tyr	His	Asp	Ala	Pro	Ile	Val	Gly	Ile	Ala	Val
	35								40						45
Val	Asn	Glu	His	Gly	Arg	Phe	Phe	Leu	Arg	Ala	Glu	Leu	Ala	Leu	Ala
	50								55						60
Ser	Pro	Gln	Phe	Val	Ala	Trp	Leu	Gly	Asp	Glu	Thr	Lys	Lys	Lys	Ser
65									70						80
Met	Phe	Asp	Ser	Lys	Arg	Ala	Ile	Val	Ala	Leu	Lys	Trp	Lys	Gly	Ile
	85								90						95
Glu	Leu	Cys	Gly	Val	Asp	Phe	Asp	Leu	Leu	Leu	Ala	Tyr	Leu	Leu	
	100								105						110
Asp	Pro	Ala	Gln	Thr	Asp	Asp	Asp	Ala	Ala	Ala	Lys	Ala	Lys	Met	Lys
	115								120						125
Gln	Tyr	His	Ala	Val	Arg	Pro	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Ala
	130								135						140
Lys	Arg	Ala	Val	Pro	Asp	Glu	Pro	Val	Leu	Ala	Glu	His	Leu	Val	Arg
145									150						160
Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Glu	Pro	Phe	Leu	Asp	Glu	Leu
	165								170						175
Arg	Arg	Asn	Glu	Gln	Asp	Arg	Leu	Leu	Ile	Glu	Leu	Glu	Met	Pro	Leu
	180								185						190
Ser	Ser	Ile	Leu	Ala	Glu	Met	Glu	Phe	Ala	Gly	Val	Lys	Val	Asp	Thr
	195								200						205
Lys	Arg	Leu	Glu	Gln	Met	Gly	Glu	Glu	Leu	Ala	Glu	Gln	Leu	Arg	Thr
	210								215						220
Val	Glu	Gln	Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile	Asn
225									230						240
Ser	Pro	Lys	Gln	Leu	Gly	Leu	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu	Pro
	245								250						255
Val	Leu	Lys	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val	Leu
	260								265						270
Glu	Lys	Leu	Ala	Pro	Tyr	His	Glu	Ile	Val	Glu	Asn	Ile	Leu	His	Tyr
	275								280						285
Arg	Gln	Leu	Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu	Gly	Leu	Leu	Lys
	290								295						300
Val	Val	His	Pro	Asp	Thr	Lys	Lys	Val	His	Thr	Ile	Phe	Asn	Gln	Ala
	305								310						320
Leu	Thr	Gln	Thr	Gly	Arg	Leu	Ser	Ser	Thr	Glu	Pro	Asn	Leu	Gln	Asn
	325								330						335
Ile	Pro	Ile	Arg	Leu	Glu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	Val
	340								345						350

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Pro Ser Glu Ser Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Glu Asp Asp Asn Leu Met Glu
 370 375 380
 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Val
 385 390 395 400
 Phe Gln Val Ser Glu Asp Glu Val Thr Pro Arg Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ser Gln Asn Leu Gly Ile Ser Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480
 Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
 485 490 495
 Phe Ala Glu Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510
 Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Asn Ala Arg Leu Lys Glu
 515 520 525
 Glu Arg Leu Gln Ala Arg Leu Leu Gln Val His Asp Glu Leu Ile
 530 535 540
 Leu Glu Ala Pro Lys Glu Glu Met Glu Arg Leu Cys Arg Leu Val Pro
 545 550 555 560
 Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
 565 570 575
 Tyr His Tyr Gly Ser Thr Trp Tyr Asp Ala Lys
 580 585

<210> SEQ_ID NO 35
 <211> LENGTH: 587
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

 <400> SEQUENCE: 35

Ala	Glu	Glu	Glu	Pro	Leu	Glu	Glu	Met	Glu	Phe	Ala	Ile	Ala	Asp
1				5			10					15		

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60

Ser Pro Gln Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

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Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Asn Asn Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu
180 185 190

Ala Ala Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu
210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu
370 375 380

Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
385 390 395 400

Phe His Val Ser Glu Asp Glu Val Thr Ala Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ser Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
435 440 445

Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

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Leu	Glu	Ala	Pro	Lys	Glu	Glu	Ile	Glu	Arg	Leu	Cys	Lys	Leu	Val	Pro
545				550				555				560			
Glu	Val	Met	Glu	Gln	Ala	Val	Glu	Leu	Arg	Val	Pro	Leu	Lys	Val	Asp
	565					570			575						
Tyr	His	Tyr	Gly	Pro	Thr	Trp	Tyr	Asp	Ala	Lys					
							580		585						

<210> SEQ_ID NO 36
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 36

Ala	Glu	Glu	Glu	Lys	Pro	Leu	Glu	Asp	Ile	Glu	Phe	Glu	Ile	Ala	Asp
1					5			10				15			
Glu	Val	Thr	Glu	Glu	Met	Leu	Ala	Asp	Glu	Ala	Ala	Leu	Val	Val	Glu
	20					25				30					
Val	Leu	Glu	Glu	Asn	Tyr	His	Asp	Ala	Pro	Ile	Val	Gly	Phe	Ala	Leu
	35					40				45					
Val	Asn	Glu	His	Gly	Arg	Phe	Phe	Ile	Arg	Thr	Glu	Thr	Ala	Leu	Ala
	50					55			60						
Ser	Ser	Gln	Phe	Lys	Ala	Trp	Leu	Glu	Asp	Glu	Thr	Lys	Lys	Lys	Ser
	65					70			75			80			
Val	Phe	Asp	Ala	Lys	Arg	Ala	Ile	Val	Ala	Leu	Lys	Trp	Lys	Gly	Ile
	85					90			95						
Glu	Leu	Arg	Gly	Val	Asp	Phe	Asp	Leu	Leu	Leu	Ala	Tyr	Leu	Leu	
	100					105			110						
Asn	Pro	Ala	Gln	Ser	Ala	Gly	Asp	Val	Ala	Ala	Val	Ala	Lys	Met	Lys
	115					120			125						
Gln	Tyr	Glu	Ala	Val	Arg	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Ala
	130					135			140						
Lys	Arg	Ala	Val	Pro	Asp	Glu	Pro	Thr	Leu	Ala	Glu	His	Leu	Val	Arg
	145					150			155			160			
Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Pro	Phe	Ile	Asp	Glu	Leu	
	165					170			175						
Arg	Glu	Asn	Glu	Gln	Asp	Glu	Leu	Phe	Thr	Glu	Leu	Glu	Met	Pro	Leu
	180					185			190						
Ala	Leu	Ile	Leu	Ala	Glu	Met	Glu	Phe	Thr	Gly	Val	Lys	Val	Asp	Thr
	195					200			205						
Lys	Arg	Leu	Glu	Gln	Met	Gly	Glu	Glu	Leu	Ala	Glu	Gln	Leu	Lys	Ala
	210					215			220						
Ile	Glu	Gln	Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile	Asn
	225					230			235			240			
Ser	Pro	Lys	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu	Pro
	245					250			255						
Val	Leu	Lys	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val	Leu
	260					265			270						
Glu	Lys	Leu	Ala	Pro	His	His	Glu	Ile	Val	Glu	Asn	Ile	Leu	His	Tyr
	275					280			285						
Arg	Gln	Leu	Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu	Gly	Leu	Leu	Lys
	290					295			300						
Val	Val	His	Pro	Asp	Thr	Gly	Lys	Val	His	Thr	Met	Phe	Asn	Gln	Ala
	305					310			315			320			

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Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asn Asp Glu Asn Leu Ile Glu
 370 375 380
 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400
 Phe His Val Ser Glu Asp Glu Val Thr Ala Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ser Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asp Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480
 Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
 485 490 495
 Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510
 Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
 515 520 525
 Glu Arg Leu Gln Ala Arg Leu Leu Gln Val His Asp Glu Leu Ile
 530 535 540
 Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro
 545 550 555 560
 Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
 565 570 575
 Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
 580 585

<210> SEQ ID NO 37
 <211> LENGTH: 587
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 37

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Val Ile Ala Asp
 1 5 10 15
 Glu Ile Thr Asp Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30
 Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45
 Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60
 Ser Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80
 Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

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Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110
 Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125
 Gln Tyr Glu Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140
 Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160
 Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
 165 170 175
 Arg Arg Asn Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu
 180 185 190
 Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
 195 200 205
 Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Lys Glu
 210 215 220
 Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240
 Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255
 Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270
 Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285
 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val His Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
 370 375 380
 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400
 Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480
 Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
 485 490 495
 Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510
 Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu

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515	520	525
Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile		
530	535	540
Leu Glu Ala Pro Lys Glu Glu Met Glu Arg Leu Cys Lys Leu Val Pro		
545	550	555
Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp		
565	570	575
Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys		
580	585	

<210> SEQ_ID NO 38

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 38

Ala Glu Gly Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Val Asp			
1	5	10	15
Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu			
20	25	30	
Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu			
35	40	45	
Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala			
50	55	60	
Asp Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser			
65	70	75	80
Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile			
85	90	95	
Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu			
100	105	110	
Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys			
115	120	125	
Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala			
130	135	140	
Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg			
145	150	155	160
Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Ile Asp Glu Leu			
165	170	175	
Arg Arg Asn Glu Gln Asp Glu Leu Leu Thr Lys Leu Glu Gln Pro Leu			
180	185	190	
Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr			
195	200	205	
Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Gly Ala			
210	215	220	
Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn			
225	230	235	240
Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro			
245	250	255	
Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asn Val Leu			
260	265	270	
Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr			
275	280	285	
Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys			

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290	295	300
Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala		
305	310	315
Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn		
325	330	335
Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val		
340	345	350
Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile		
355	360	365
Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu		
370	375	380
Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile		
385	390	395
Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala		
405	410	415
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu		
420	425	430
Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu		
435	440	445
Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile		
450	455	460
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg		
465	470	475
480		
Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser		
485	490	495
Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala		
500	505	510
Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu		
515	520	525
Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile		
530	535	540
Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro		
545	550	555
560		
Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp		
565	570	575
Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys		
580	585	

<210> SEQ ID NO 39

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 39

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp		
1	5	10
		15
Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu		
20	25	30
Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu		
35	40	45
Val Asn Glu His Gly Arg Phe Phe Leu Arg Thr Glu Thr Ala Leu Ala		
50	55	60
Asp Pro Gln Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser		

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65	70	75	80
Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile			
85	90	95	
Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu			
100	105	110	
Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys			
115	120	125	
Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala			
130	135	140	
Lys Arg Ala Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg			
145	150	155	160
Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Leu Asp Glu Leu			
165	170	175	
Arg Glu Asn Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu			
180	185	190	
Ala Leu Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr			
195	200	205	
Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Ala			
210	215	220	
Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn			
225	230	235	240
Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro			
245	250	255	
Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu			
260	265	270	
Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr			
275	280	285	
Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys			
290	295	300	
Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala			
305	310	315	320
Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn			
325	330	335	
Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val			
340	345	350	
Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile			
355	360	365	
Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu			
370	375	380	
Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile			
385	390	395	400
Phe His Val Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala			
405	410	415	
Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu			
420	425	430	
Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu			
435	440	445	
Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asp Ile			
450	455	460	
Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg			
465	470	475	480
Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser			
485	490	495	

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Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 40

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 40

Ala Glu Asp Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp
1 5 10 15

Gly Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Glu Leu
165 170 175

Arg Ser Asn Glu Gln Asp Gln Leu Leu Thr Lys Leu Glu Gln Pro Leu
180 185 190

Ala Ser Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
195 200 205

Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala
210 215 220

Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

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Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285
 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu
 370 375 380
 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400
 Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480
 Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
 485 490 495
 Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510
 Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
 515 520 525
 Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
 530 535 540
 Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro
 545 550 555 560
 Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
 565 570 575
 Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
 580 585

<210> SEQ ID NO 41
 <211> LENGTH: 587
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 41

Ala Glu Glu Glu Lys Pro Leu Glu Glu Met Glu Phe Ala Ile Ala Asp
 1 5 10 15
 Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30
 Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

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Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60
 Asp Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80
 Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95
 Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
 100 105 110
 Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125
 Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140
 Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
 145 150 155 160
 Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
 165 170 175
 Arg Arg Asn Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu
 180 185 190
 Ala Thr Ile Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr
 195 200 205
 Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu
 210 215 220
 Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
 225 230 235 240
 Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
 245 250 255
 Val Leu Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270
 Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285
 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val His Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
 370 375 380
 Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400
 Phe His Val Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile
 450 455 460

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Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
515 520 525

Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro
545 550 555 560

Glu Val Met Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp
565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 42

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 42

Glu Glu Glu Glu Pro Leu Glu Asp Ile Ser Phe Glu Ile Val Glu
1 5 10 15

Glu Val Thr Glu Asp Met Leu Thr Asp Glu Ser Ala Leu Val Val Glu
20 25 30

Val Leu Glu Glu Asn Tyr His Lys Ala Asp Ile Val Gly Phe Ala Ile
35 40 45

Ala Asn Glu Asn Gly Asn Phe Phe Ile Pro Thr Asp Thr Ala Leu Ala
50 55 60

Ser Glu Ala Phe Lys Lys Trp Leu Glu Asp Glu Thr Lys Lys Ser
65 70 75 80

Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp His Gly Ile
85 90 95

Glu Leu Lys Gly Val Asp Phe Asp Leu Leu Ile Ala Ser Tyr Leu Leu
100 105 110

Asn Pro Ser Glu Ser Ser Asp Asp Phe Ala Ser Val Ala Lys Thr Lys
115 120 125

Gly Tyr Asn Ala Val Gln Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Asp Glu Glu Lys Leu Ala Glu His Leu Ala Arg
145 150 155 160

Lys Ala Ala Ala Ile Ser Ala Leu Lys Glu Thr Phe Ile His Glu Leu
165 170 175

Lys Glu Asn Glu Gln Tyr Glu Leu Phe Thr Asp Leu Glu Met Pro Leu
180 185 190

Ala Leu Ile Leu Ala Asp Met Glu Tyr Thr Gly Val Lys Val Asp Val
195 200 205

Glu Arg Leu Lys Glu Met Gly Glu Glu Leu Thr Glu Arg Leu Lys Glu
210 215 220

Ile Glu Gln Lys Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240

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Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gly Leu Pro
245 250 255

Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270

Glu Lys Leu Ala Ser His His Glu Ile Ile Arg His Ile Leu His Tyr
275 280 285

Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
290 295 300

Val Val His Glu Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala
305 310 315 320

Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn
325 330 335

Ile Pro Ile Arg Leu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
340 345 350

Pro Ser Glu Pro Gly Trp Val Ile Phe Ala Ala Asp Tyr Ser Gln Ile
355 360 365

Glu Leu Arg Val Leu Ala His Ile Ala Asn Asp Glu Asn Leu Ile Glu
370 375 380

Ala Phe Arg His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val
385 390 395 400

Phe His Val Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala
405 410 415

Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
420 425 430

Ser Gln Asn Leu Gly Ile Thr Arg Lys Glu Ala Gly Glu Phe Ile Glu
435 440 445

Arg Tyr Leu Glu Ser Phe Pro Gly Val Lys Glu Tyr Met Asp Asp Ile
450 455 460

Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
465 470 475 480

Arg Arg Tyr Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser
485 490 495

Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
500 505 510

Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Asp Arg Leu Lys Glu
515 520 525

Glu Asn Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
530 535 540

Phe Glu Ala Pro Lys Glu Glu Ile Glu Lys Leu Lys Lys Ile Val Pro
545 550 555 560

Glu Val Met Glu Asn Ala Val Glu Leu Lys Val Pro Leu Lys Val Asp
565 570 575

Tyr Ser Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
580 585

<210> SEQ ID NO 43
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 43

Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Ser Ile
1 5 10 15

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Leu Ala Glu Met Glu Phe Thr Gly Val Asn Val Asp Thr Lys Arg Leu
 20 25 30
 Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Lys Glu Gln Glu Gln
 35 40 45
 Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60
 Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80
 Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95
 Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110
 Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125
 Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
 130 135 140
 Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160
 Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175
 Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190
 Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Gln
 195 200 205
 Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
 210 215 220
 Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240
 Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
 245 250 255
 Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
 260 265 270
 Ala Ser Phe Pro Gly Val Lys Glu Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285
 Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300
 Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320
 Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335
 Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Gln Leu
 340 345 350
 Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365
 Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met
 370 375 380
 Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400
 Gly Pro Thr Trp Tyr Asp Ala Lys
 405

<210> SEQ_ID NO 44
 <211> LENGTH: 408
 <212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 44

Glu	Gln	Tyr	Glu	Leu	Leu	Thr	Glu	Leu	Glu	Met	Pro	Leu	Ala	Leu	Ile
1				5			10			15					

Leu	Ala	Asp	Met	Glu	Tyr	Thr	Gly	Val	Lys	Val	Asp	Val	Glu	Arg	Leu
			20			25			30						

Lys	Glu	Met	Gly	Glu	Glu	Leu	Thr	Glu	Arg	Leu	Lys	Glu	Ile	Glu	Gln
	35				40			45							

Lys	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile	Asn	Ser	Pro	Lys
	50				55			60							

Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gly	Leu	Pro	Val	Ile	Lys
65				70			75			80					

Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val	Leu	Glu	Lys	Leu
	85				90			95							

Ala	Ser	His	His	Glu	Ile	Ile	Arg	His	Ile	Leu	His	Tyr	Arg	Gln	Leu
			100				105			110					

Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu	Gly	Leu	Leu	Lys	Val	Val	His
	115				120			125							

Pro	Asp	Thr	Gly	Lys	Val	His	Thr	Arg	Phe	Asn	Gln	Ala	Leu	Thr	Gln
	130				135			140							

Thr	Gly	Arg	Leu	Ser	Ser	Thr	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Ile
145				150			155			160					

Arg	Leu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	Val	Pro	Ser	Glu
	165				170			175						

Pro	Gly	Trp	Val	Ile	Phe	Ala	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg
	180				185			190							

Val	Leu	Ala	His	Ile	Ala	Asn	Asp	Glu	Asn	Leu	Ile	Glu	Ala	Phe	Arg
	195				200			205							

His	Asp	Met	Asp	Ile	His	Thr	Lys	Thr	Ala	Met	Asp	Val	Phe	His	Val
	210				215			220							

Ser	Glu	Asp	Glu	Val	Thr	Ser	Asn	Met	Arg	Arg	Gln	Ala	Lys	Ala	Val
225				230			235			240					

Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile	Ser	Asp	Tyr	Gly	Leu	Ser	Gln	Asn
	245				250			255			255				

Leu	Gly	Ile	Thr	Arg	Lys	Glu	Ala	Gly	Glu	Phe	Ile	Glu	Arg	Tyr	Leu
	260			265			270								

Glu	Ser	Phe	Pro	Gly	Val	Lys	Glu	Tyr	Met	Asp	Asp	Ile	Val	Gln	Glu
	275				280			285							

Ala	Lys	Gln	Lys	Gly	Tyr	Val	Thr	Leu	Leu	His	Arg	Arg	Tyr	
	290				295			300						

Leu	Pro	Glu	Ile	Thr	Ser	Arg	Asn	Phe	Asn	Leu	Arg	Ser	Phe	Ala	Glu
305				310			315			320					

Arg	Thr	Ala	Met	Asn	Thr	Pro	Ile	Gln	Gly	Ser	Ala	Ala	Asp	Ile	Ile
	325				330			335							

Lys	Lys	Ala	Met	Ile	Asp	Met	Ala	Asp	Arg	Leu	Lys	Glu	Glu	Asn	Leu
	340				345			350							

Gln	Ala	Arg	Leu	Leu	Leu	Gln	Val	His	Asp	Glu	Leu	Ile	Phe	Glu	Ala
	355				360			365							

Pro	Lys	Glu	Ile	Glu	Lys	Leu	Cys	Lys	Leu	Val	Pro	Glu	Val	Met
	370				375			380						

Glu Asn Ala Val Glu Leu Lys Val Pro Leu Lys Val Asp Tyr Ser Tyr

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385	390	395	400
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Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ_ID NO 45
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 45

Glu Gln Asp Glu Leu Phe Thr Lys Leu Glu Gln Pro Leu Ala Thr Ile
1 5 10 15

Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
20 25 30

Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln
35 40 45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95

Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115 120 125

Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
130 135 140

Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile
145 150 155 160

Arg Leu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165 170 175

Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180 185 190

Val Leu Ala His Ile Ala Asp Asp Glu Asn Leu Ile Glu Ala Phe Arg
195 200 205

Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
210 215 220

Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
245 250 255

Leu Asn Ile Lys Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260 265 270

Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
305 310 315 320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335

Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu

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340	345	350
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala		
355	360	365
Pro Lys Glu Glu Ile Glu Arg Leu Glu Gln Leu Val Pro Glu Val Met		
370	375	380
Glu Gln Ala Val Arg Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr		
385	390	395
Gly Pro Thr Trp Tyr Asp Ala Lys		
405		

<210> SEQ_ID NO 46

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 46

Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Leu Ile		
1	5	10
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu		
20	25	30
Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln		
35	40	45
Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys		
50	55	60
Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys		
65	70	75
Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu		
85	90	95
Ala Pro His Arg Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu		
100	105	110
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His		
115	120	125
Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln		
130	135	140
Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile		
145	150	155
Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu		
165	170	175
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg		
180	185	190
Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg		
195	200	205
Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val		
210	215	220
Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val		
225	230	235
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn		
245	250	255
Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe		
260	265	270
Gln Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asp Ile Val Gln Glu		
275	280	285
Ala Lys Gln Lys Gly Tyr Val Thr Leu Leu His Arg Arg Arg Tyr		

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290	295	300
Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu		
305	310	315
Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile		
325	330	335
Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu		
340	345	350
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala		
355	360	365
Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met		
370	375	380
Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr Arg Tyr		
385	390	395
Gly Pro Thr Trp Tyr Asp Ala Lys		
405		

<210> SEQ ID NO: 47

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 47

Glu Gln Asp Glu Leu Phe Thr Glu Leu Glu Leu Pro Leu Ala Leu Ile		
1	5	10
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu		
20	25	30
Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln		
35	40	45
Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys		
50	55	60
Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys		
65	70	75
Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu		
85	90	95
Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu		
100	105	110
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His		
115	120	125
Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln		
130	135	140
Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Ile		
145	150	155
Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu		
165	170	175
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg		
180	185	190
Val Leu Ala His Ile Ala Asn Asp Asp Asn Leu Ile Glu Ala Phe Arg		
195	200	205
Arg Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val Phe His Val		
210	215	220
Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala Lys Ala Val		
225	230	235
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn		

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245	250	255
Leu Gly Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe		
260	265	270
Glu Ser Phe Pro Gly Val Lys Glu Tyr Met Glu Asp Ile Val Gln Glu		
275	280	285
Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr		
290	295	300
Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser Phe Ala Glu		
305	310	315
Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile		
325	330	335
Lys Lys Ala Met Ile Asp Met Ala Ala Arg Leu Lys Glu Glu Arg Leu		
340	345	350
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Phe Glu Ala		
355	360	365
Pro Lys Glu Glu Ile Glu Arg Leu Glu Lys Leu Val Pro Glu Val Met		
370	375	380
Glu His Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr		
385	390	395
Gly Pro Thr Trp Tyr Asp Ala Lys		
405		

<210> SEQ ID NO 48

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 48

Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Thr Ile		
1	5	10
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu		
20	25	30
Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala Val Glu Gln		
35	40	45
Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys		
50	55	60
Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys		
65	70	75
Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu		
85	90	95
Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu		
100	105	110
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His		
115	120	125
Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln		
130	135	140
Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile		
145	150	155
Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu		
165	170	175
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg		
180	185	190
Val Leu Ala His Ile Ala Asn Asp Asn Leu Ile Glu Ala Phe Arg		

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195 200 205

Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Val Phe His Val
 210 215 220

Ser Glu Glu Glu Val Thr Ala Arg Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
 245 250 255

Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
 260 265 270

Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320

Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335

Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
 340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365

Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met
 370 375 380

Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
 405

<210> SEQ ID NO 49

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 49

Glu Gln Asp Gln Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Ala Ile
 1 5 10 15

Leu Ala Glu Met Glu Phe Thr Gly Val Asn Val Asp Thr Lys Arg Leu
 20 25 30

Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Lys Glu Ile Glu Gln
 35 40 45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95

Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125

Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
 130 135 140

Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile

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145	150	155	160
Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu			
165	170	175	
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg			
180	185	190	
Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Gln			
195	200	205	
Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val			
210	215	220	
Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val			
225	230	235	240
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn			
245	250	255	
Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe			
260	265	270	
Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile Val Gln Glu			
275	280	285	
Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr			
290	295	300	
Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu			
305	310	315	320
Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile			
325	330	335	
Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Gln Leu			
340	345	350	
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala			
355	360	365	
Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met			
370	375	380	
Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr			
385	390	395	400
Gly Pro Thr Trp Tyr Asp Ala Lys			
405			

<210> SEQ ID NO 50
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 50

Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Thr Ile			
1	5	10	15
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu			
20	25	30	
Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln			
35	40	45	
Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys			
50	55	60	
Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys			
65	70	75	80
Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu			
85	90	95	
Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu			

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100	105	110
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His		
115	120	125
Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln		
130	135	140
Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile		
145	150	155
Arg Leu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu		
165	170	175
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg		
180	185	190
Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg		
195	200	205
Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val		
210	215	220
Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val		
225	230	235
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn		
245	250	255
Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe		
260	265	270
Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu		
275	280	285
Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr		
290	295	300
Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu		
305	310	315
Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile		
325	330	335
Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu		
340	345	350
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala		
355	360	365
Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met		
370	375	380
Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr		
385	390	395
Gly Pro Thr Trp Tyr Asp Ala Lys		
405		

<210> SEQ_ID NO 51
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 51

Glu Gln Asp Gln Leu Leu Thr Lys Leu Glu Gln Pro Leu Ala Ser Ile		
1	5	10
15		
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu		
20	25	30
Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala Val Glu Gln		
35	40	45
Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys		

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50	55	60
Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys		
65	70	75
Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu		
85	90	95
Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu		
100	105	110
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His		
115	120	125
Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln		
130	135	140
Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile		
145	150	155
Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu		
165	170	175
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg		
180	185	190
Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg		
195	200	205
Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val		
210	215	220
Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val		
225	230	235
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn		
245	250	255
Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe		
260	265	270
Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile Val Gln Glu		
275	280	285
Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr		
290	295	300
Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu		
305	310	315
Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile		
325	330	335
Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu		
340	345	350
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala		
355	360	365
Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met		
370	375	380
Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr		
385	390	395
Gly Pro Thr Trp Tyr Asp Ala Lys		
405		

<210> SEQ_ID NO 52

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 52

Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Thr Ile

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1	5	10	15
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu			
20	25	30	
Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln			
35	40	45	
Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys			
50	55	60	
Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys			
65	70	75	80
Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu			
85	90	95	
Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu			
100	105	110	
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His			
115	120	125	
Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln			
130	135	140	
Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile			
145	150	155	160
Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu			
165	170	175	
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg			
180	185	190	
Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg			
195	200	205	
Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val			
210	215	220	
Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val			
225	230	235	240
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn			
245	250	255	
Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe			
260	265	270	
Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu			
275	280	285	
Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr			
290	295	300	
Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu			
305	310	315	320
Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile			
325	330	335	
Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu			
340	345	350	
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala			
355	360	365	
Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met			
370	375	380	
Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr			
385	390	395	400
Gly Pro Thr Trp Tyr Asp Ala Lys			
405			

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<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 53

Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Thr Ile
1           5          10          15

Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
20          25          30

Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln
35          40          45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
50          55          60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
65          70          75          80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85          90          95

Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
100         105         110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115         120         125

Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
130         135         140

Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile
145         150         155         160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165         170         175

Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180         185         190

Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
195         200         205

Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
210         215         220

Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
225         230         235         240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
245         250         255

Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260         265         270

Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
275         280         285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290         295         300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
305         310         315         320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325         330         335

Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
340         345         350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
355         360         365

Pro Lys Glu Glu Met Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met
370         375         380

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Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
 405

<210> SEQ ID NO 54

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 54

Asp Gln Tyr Glu Leu Leu Thr Glu Leu Glu Met Pro Leu Ala Leu Ile
 1 5 10 15

Leu Gly Glu Met Glu Ser Thr Gly Val Lys Val Asp Val Glu Arg Leu
 20 25 30

Lys Arg Met Gly Glu Glu Leu Thr Glu Lys Leu Lys Glu Tyr Glu Glu
 35 40 45

Lys Ile His Glu Leu Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys
 50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gly Leu Pro Val Ile Lys
 65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95

Ala Asp Lys His Glu Ile Ile Arg Tyr Ile Leu His Tyr Arg Gln Ile
 100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Thr Arg
 115 120 125

Lys Asp Thr His Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
 130 135 140

Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175

Glu Gly Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190

Val Leu Ala His Ile Ser Lys Asp Glu Asn Leu Ile Glu Ala Phe Thr
 195 200 205

His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val Phe His Val
 210 215 220

Ser Glu Asp Glu Val Thr Ser Ala Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn
 245 250 255

Leu Gly Ile Thr Arg Lys Glu Ala Gly Ala Phe Ile Glu Arg Tyr Leu
 260 265 270

Glu Ser Phe Pro Gly Val Lys Ala Tyr Met Glu Asp Ile Val Gln Glu
 275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300

Ile Pro Glu Ile Thr Ser Arg Asn Phe Asn Ile Arg Ser Phe Ala Glu
 305 310 315 320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335

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Lys Lys Ala Met Ile Asp Met Ala Ala Arg Leu Lys Glu Glu Asn Leu
340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Phe Glu Ala
355 360 365

Pro Lys Glu Glu Ile Glu Ile Leu Cys Lys Leu Val Pro Glu Val Met
370 375 380

Glu His Ala Val Glu Leu Asp Val Pro Leu Lys Val Asp Tyr Ala Ser
385 390 395 400

Gly Pro Ser Trp Tyr Asp Ala Lys
405

<210> SEQ ID NO 55

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 55

Glu Gln Tyr Glu Leu Leu Thr Glu Leu Glu Met Pro Leu Ala Leu Ile
1 5 10 15

Leu Ala Asp Met Glu Tyr Thr Gly Val Lys Val Asp Val Glu Arg Leu
20 25 30

Lys Glu Met Gly Glu Glu Leu Ala Glu Arg Leu Lys Glu Ile Glu Gln
35 40 45

Lys Ile Tyr Glu Leu Ala Gly Glu Glu Phe Asn Ile Asn Ser Pro Lys
50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gly Leu Pro Val Ile Lys
65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95

Ala Ser Lys His Glu Ile Ile Arg Asn Ile Leu His Tyr Arg Gln Leu
100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115 120 125

Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
130 135 140

Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Ile
145 150 155 160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165 170 175

Glu Gly Trp Val Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180 185 190

Val Leu Ala His Ile Ala Asn Asp Glu Lys Leu Ile Glu Ala Phe Arg
195 200 205

His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val Phe His Val
210 215 220

Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn
245 250 255

Leu Gly Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Leu
260 265 270

Glu Ser Phe Pro Gly Val Lys Glu Tyr Met Asp Asp Ile Val Gln Glu
275 280 285

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Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Arg Tyr
 290 295 300
 Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser Phe Ala Glu
 305 310 315 320
 Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335
 Lys Lys Ala Met Ile Asp Met Ala Asn Arg Leu Lys Glu Glu Asn Leu
 340 345 350
 Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Phe Glu Ala
 355 360 365
 Pro Lys Glu Glu Ile Glu Lys Cys Lys Ile Val Pro Glu Val Met
 370 375 380
 Glu His Ala Val Glu Leu Lys Val Pro Leu Lys Val Asp Tyr Ser Tyr
 385 390 395 400
 Gly Pro Thr Trp Tyr Asp Ala Lys
 405

<210> SEQ ID NO 56
 <211> LENGTH: 408
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct
 <400> SEQUENCE: 56

Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Ser Ile
 1 5 10 15
 Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
 20 25 30
 Glu Gln Met Gly Glu Glu Leu Thr Glu Gln Leu Lys Glu Val Glu Gln
 35 40 45
 Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60
 Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80
 Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95
 Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110
 Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125
 Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
 130 135 140
 Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160
 Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175
 Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190
 Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
 195 200 205
 Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
 210 215 220
 Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240

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Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
 245 250 255
 Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
 260 265 270
 Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285
 Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300
 Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320
 Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335
 Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
 340 345 350
 Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365
 Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met
 370 375 380
 Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400
 Gly Pro Thr Trp Tyr Asp Ala Lys
 405

<210> SEQ_ID NO 57
 <211> LENGTH: 408
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

 <400> SEQUENCE: 57

Glu	Gln	Asp	Arg	Leu	Leu	Val	Glu	Leu	Glu	Met	Pro	Leu	Ser	Ser	Ile
1				5			10			15					

Leu Ala Glu Met Glu Phe Ala Gly Val Lys Val Asp Thr Lys Arg Leu
 20 25 30

Glu	Gln	Met	Gly	Glu	Glu	Leu	Ala	Glu	Gln	Leu	Arg	Thr	Val	Glu	Gln
35				40			45								

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60

Gln	Leu	Gly	Leu	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu	Pro	Val	Leu	Lys
65				70			75			80					

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95

Ala	Pro	Tyr	His	Glu	Ile	Val	Glu	Asn	Ile	Leu	His	Tyr	Arg	Gln	Leu
100				105			110								

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125

Pro	Asp	Thr	Lys	Lys	Val	His	Thr	Ile	Phe	Asn	Gln	Ala	Leu	Thr	Gln
130				135			140								

Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160

Arg	Leu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	Val	Pro	Ser	Glu
165				170			175							

Ser Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190

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Val Leu Ala His Ile Ala Glu Asp Asp Asn Leu Met Glu Ala Phe Arg
195 200 205

Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Val Phe Gln Val
210 215 220

Ser Glu Asp Glu Val Thr Pro Arg Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn
245 250 255

Leu Gly Ile Ser Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260 265 270

Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
305 310 315 320

Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335

Lys Lys Ala Met Ile Asp Leu Asn Ala Arg Leu Lys Glu Arg Leu
340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
355 360 365

Pro Lys Glu Glu Met Glu Arg Leu Cys Arg Leu Val Pro Glu Val Met
370 375 380

Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
385 390 395 400

Gly Ser Thr Trp Tyr Asp Ala Lys
405

<210> SEQ ID NO 58

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 58

Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Leu Ile
1 5 10 15

Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
20 25 30

Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln
35 40 45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95

Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115 120 125

Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln
130 135 140

-continued

Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160
 Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175
 Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190
 Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
 195 200 205
 Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
 210 215 220
 Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240
 Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
 245 250 255
 Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
 260 265 270
 Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285
 Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300
 Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320
 Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335
 Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
 340 345 350
 Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365
 Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met
 370 375 380
 Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400
 Gly Pro Thr Trp Tyr Asp Ala Lys
 405

<210> SEQ ID NO 59
 <211> LENGTH: 408
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

 <400> SEQUENCE: 59

 Glu Gln Asp Glu Leu Leu Thr Asp Leu Glu Gln Pro Leu Ser Ser Ile
 1 5 10 15

 Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
 20 25 30

 Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Arg Ala Val Glu Gln
 35 40 45

 Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60

 Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80

 Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95

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Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110
 Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125
 Pro Asp Thr Gly Lys Val His Thr Ile Phe Asn Gln Ala Leu Thr Gln
 130 135 140
 Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160
 Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175
 Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190
 Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
 195 200 205
 Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
 210 215 220
 Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240
 Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
 245 250 255
 Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
 260 265 270
 Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285
 Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300
 Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320
 Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335
 Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
 340 345 350
 Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365
 Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met
 370 375 380
 Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400
 Gly Pro Thr Trp Tyr Asp Ala Lys
 405

<210> SEQ_ID NO 60
 <211> LENGTH: 408
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

 <400> SEQUENCE: 60

 Glu Gln Asp Glu Leu Leu Ile Lys Leu Glu Gln Pro Leu Ala Thr Ile
 1 5 10 15

 Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
 20 25 30

 Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala Val Glu Gln
 35 40 45

-continued

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60
 Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80
 Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95
 Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110
 Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125
 Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln
 130 135 140
 Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160
 Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175
 Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190
 Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
 195 200 205
 Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
 210 215 220
 Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240
 Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
 245 250 255
 Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
 260 265 270
 Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285
 Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300
 Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320
 Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335
 Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
 340 345 350
 Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365
 Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met
 370 375 380
 Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400
 Gly Pro Thr Trp Tyr Asp Ala Lys
 405

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<210> SEQ_ID NO 61
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 61
  
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Glu Gln Asp Glu Leu Leu Thr Lys Leu Glu Gln Pro Leu Ala Thr Ile
 1 5 10 15
 Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
 20 25 30
 Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Gly Ala Val Glu Gln
 35 40 45
 Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60
 Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80
 Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95
 Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110
 Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125
 Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln
 130 135 140
 Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160
 Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175
 Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190
 Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
 195 200 205
 Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
 210 215 220
 Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240
 Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
 245 250 255
 Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
 260 265 270
 Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285
 Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300
 Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320
 Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335
 Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
 340 345 350
 Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365
 Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met
 370 375 380
 Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400
 Gly Pro Thr Trp Tyr Asp Ala Lys
 405

-continued

<210> SEQ ID NO 62
 <211> LENGTH: 408
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

 <400> SEQUENCE: 62

Glu	Gln	Asp	Arg	Leu	Leu	Thr	Asp	Leu	Glu	Gln	Pro	Leu	Ser	Ser	Ile
1				5				10				15			
Leu	Ala	Glu	Met	Glu	Phe	Thr	Gly	Val	Lys	Val	Asp	Thr	Lys	Arg	Leu
	20				25				30						
Glu	Gln	Met	Gly	Glu	Glu	Leu	Ala	Glu	Gln	Leu	Arg	Ala	Val	Glu	Gln
	35				40				45						
Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile	Asn	Ser	Pro	Lys
	50				55				60						
Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu	Pro	Val	Leu	Lys
	65				70				75			80			
Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val	Leu	Glu	Lys	Leu
	85				90				95						
Ala	Pro	His	His	Ile	Val	Glu	Asn	Ile	Leu	His	Tyr	Arg	Gln	Leu	
	100				105				110						
Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu	Gly	Leu	Leu	Lys	Val	Val	His
	115				120				125						
Pro	Asp	Thr	Gly	Lys	Val	His	Thr	Ile	Phe	Asn	Gln	Ala	Leu	Thr	Gln
	130				135				140						
Thr	Gly	Arg	Leu	Ser	Ser	Thr	Glu	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Ile
	145				150				155			160			
Arg	Leu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	Val	Pro	Ser	Glu	
	165				170				175						
Pro	Asp	Trp	Leu	Ile	Phe	Ala	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg
	180				185				190						
Val	Leu	Ala	His	Ile	Ala	Asn	Asp	Asp	Asn	Leu	Ile	Glu	Ala	Phe	Arg
	195				200				205						
Arg	Asp	Leu	Asp	Ile	His	Thr	Lys	Thr	Ala	Met	Asp	Ile	Phe	His	Val
	210				215				220						
Ser	Glu	Asp	Glu	Val	Thr	Ala	Asn	Met	Arg	Arg	Gln	Ala	Lys	Ala	Val
	225				230				235			240			
Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile	Ser	Asp	Tyr	Gly	Leu	Ala	Gln	Asn
	245				250				255						
Leu	Asn	Ile	Thr	Arg	Lys	Glu	Ala	Ala	Glu	Phe	Ile	Glu	Arg	Tyr	Phe
	260				265				270						
Glu	Ser	Phe	Pro	Gly	Val	Lys	Gln	Tyr	Met	Glu	Asn	Ile	Val	Gln	Glu
	275				280				285						
Ala	Lys	Gln	Lys	Gly	Tyr	Val	Thr	Thr	Leu	Leu	His	Arg	Arg	Arg	Tyr
	290				295				300						
Leu	Pro	Asp	Ile	Thr	Ser	Arg	Asn	Phe	Asn	Val	Arg	Ser	Phe	Ala	Glu
	305				310				315			320			
Arg	Thr	Ala	Met	Asn	Thr	Pro	Ile	Gln	Gly	Ser	Ala	Ala	Asp	Ile	Ile
	325				330				335						
Lys	Lys	Ala	Met	Ile	Asp	Leu	Ala	Ala	Arg	Leu	Lys	Glu	Glu	Arg	Leu
	340				345				350						
Gln	Ala	Arg	Leu	Leu	Leu	Gln	Val	His	Asp	Glu	Leu	Ile	Leu	Glu	Ala
	355				360				365						

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Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met
370 375 380

Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ_ID NO 63

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 63

Glu Gln Tyr Glu Leu Phe Thr Asp Leu Glu Met Pro Leu Ala Leu Ile
1 5 10 15

Leu Ala Asp Met Glu Tyr Thr Gly Val Lys Val Asp Val Glu Arg Leu
20 25 30

Lys Glu Met Gly Glu Glu Leu Thr Glu Arg Leu Lys Glu Ile Glu Gln
35 40 45

Lys Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gly Leu Pro Val Ile Lys
65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95

Ala Ser His His Glu Ile Ile Arg His Ile Leu His Tyr Arg Gln Leu
100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115 120 125

Glu Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
130 135 140

Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Ile
145 150 155 160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165 170 175

Pro Gly Trp Val Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180 185 190

Val Leu Ala His Ile Ala Asn Asp Glu Asn Leu Ile Glu Ala Phe Arg
195 200 205

His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val Phe His Val
210 215 220

Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn
245 250 255

Leu Gly Ile Thr Arg Lys Glu Ala Gly Glu Phe Ile Glu Arg Tyr Leu
260 265 270

Glu Ser Phe Pro Gly Val Lys Glu Tyr Met Asp Asp Ile Val Gln Glu
275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser Phe Ala Glu
305 310 315 320

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Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335

Lys Lys Ala Met Ile Asp Met Ala Asp Arg Leu Lys Glu Glu Asn Leu
340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Phe Glu Ala
355 360 365

Pro Lys Glu Glu Ile Glu Lys Leu Lys Ile Val Pro Glu Val Met
370 375 380

Glu Asn Ala Val Glu Leu Lys Val Pro Leu Lys Val Asp Tyr Ser Tyr
385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ_ID NO 64

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 64

Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Ala Ile
1 5 10 15

Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
20 25 30

Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln
35 40 45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95

Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115 120 125

Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
130 135 140

Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
145 150 155 160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165 170 175

Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180 185 190

Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
195 200 205

Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
210 215 220

Ser Glu Asp Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn
245 250 255

Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260 265 270

229

230

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Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Leu	Pro	Asp	Ile	Thr	Ser	Arg	Asn	Phe	Asn	Val	Arg	Ser	Phe	Ala	Glut
305					310					315					320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335

Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
355 360 365

Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met
370 375 380

Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ ID NO: 65
<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 65
Glu Gln Asp Arg Leu Leu Ile Lys Leu Glu Gln Pro Leu Ala Thr Ile

1 5 10 15
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu

Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala Val Glu Gln

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys

65 70 75 80

85 90 95

100 105 110

115 120 125

130 135 140

145 150 155 160

165 170 175

180 185 190

195 200 205

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Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
245 250 255

Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260 265 270

Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
305 310 315 320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335

Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
355 360 365

Pro Lys Glu Glu Met Glu Arg Leu Cys Arg Leu Val Pro Glu Val Met
370 375 380

Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ ID NO 66
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 66

Asp Gln Tyr Glu Leu Phe Glu Asp Leu Glu Met Pro Leu Ala Leu Ile
1 5 10 15

Leu Gly Glu Met Glu Ser Thr Gly Val Lys Val Asp Val Glu Arg Leu
20 25 30

Lys Arg Met Gly Glu Glu Leu Thr Glu Lys Leu Lys Glu Tyr Glu Glu
35 40 45

Lys Ile His Glu Leu Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys
50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gly Leu Pro Val Ile Lys
65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95

Ala Asp Lys His Glu Ile Ile Arg Tyr Ile Leu His Tyr Arg Gln Ile
100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Thr Arg
115 120 125

Lys Asp Thr His Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
130 135 140

Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Ile
145 150 155 160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165 170 175

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Glu Gly Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180 185 190

Val Leu Ala His Ile Ser Lys Asp Glu Asn Leu Ile Glu Ala Phe Thr
195 200 205

His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val Phe His Val
210 215 220

Ser Glu Asp Glu Val Thr Ser Ala Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn
245 250 255

Leu Gly Ile Thr Arg Lys Glu Ala Gly Ala Phe Ile Glu Arg Tyr Leu
260 265 270

Glu Ser Phe Pro Gly Val Lys Ala Tyr Met Glu Asp Ile Val Gln Glu
275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Ile Pro Glu Ile Thr Ser Arg Asn Phe Asn Ile Arg Ser Phe Ala Glu
305 310 315 320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335

Lys Lys Ala Met Ile Asp Met Ala Ala Arg Leu Lys Glu Glu Asn Leu
340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Phe Glu Ala
355 360 365

Pro Lys Glu Glu Ile Glu Ile Leu Glu Lys Ile Val Pro Glu Val Met
370 375 380

Glu His Ala Leu Glu Leu Asp Val Pro Leu Lys Val Asp Tyr Ala Ser
385 390 395 400

Gly Pro Ser Trp Tyr Asp Ala Lys
405

<210> SEQ ID NO 67
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 67

Glu Gln Asp Arg Leu Leu Thr Lys Leu Glu Gln Pro Leu Ala Thr Ile
1 5 10 15

Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
20 25 30

Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala Val Glu Gln
35 40 45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95

Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115 120 125

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Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln
130 135 140

Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
145 150 155 160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165 170 175

Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180 185 190

Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
195 200 205

Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
210 215 220

Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
245 250 255

Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260 265 270

Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
305 310 315 320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335

Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
355 360 365

Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met
370 375 380

Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ ID NO 68
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 68

Glu Gln Asp Glu Leu Leu Thr Lys Leu Glu Gln Pro Leu Ala Leu Ile
1 5 10 15

Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
20 25 30

Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Ile Glu Gln
35 40 45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
65 70 75 80

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Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95

Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val Arg
115 120 125

Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln
130 135 140

Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
145 150 155 160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165 170 175

Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180 185 190

Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
195 200 205

Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
210 215 220

Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn
245 250 255

Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260 265 270

Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Glu Ile Val Gln Glu
275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
305 310 315 320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335

Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
355 360 365

Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met
370 375 380

Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ_ID NO 69
<211> LENGTH: 399
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 69

Glu Gln Pro Leu Ser Ser Ile Leu Ala Glu Met Glu Phe Ala Gly Val
1 5 10 15

Lys Val Asp Thr Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu
20 25 30

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Gln	Leu	Lys	Glu	Gln	Glu	Gln	Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu
35					40						45				
Phe	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys
50						55					60				
Leu	Gln	Leu	Pro	Val	Leu	Lys	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser
65						70			75						80
Ala	Asp	Val	Leu	Glu	Lys	Leu	Ala	Pro	Tyr	His	Glu	Ile	Val	Glu	Asn
								85		90					95
Ile	Leu	His	Tyr	Arg	Gln	Leu	Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu
								100		105					110
Gly	Leu	Leu	Lys	Val	Val	Arg	Pro	Asp	Thr	Lys	Lys	Val	His	Thr	Ile
						115			120						125
Phe	Asn	Gln	Ala	Leu	Thr	Gln	Thr	Gly	Arg	Leu	Ser	Ser	Thr	Glu	Pro
							130			135					140
Asn	Leu	Gln	Asn	Ile	Pro	Ile	Arg	Leu	Glu	Gly	Arg	Lys	Ile	Arg	
145						150			155						160
Gln	Ala	Phe	Val	Pro	Ser	Glu	Ser	Asp	Trp	Leu	Ile	Phe	Ala	Ala	Asp
						165			170						175
Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Ile	Ala	Glu	Asp	Glu
						180			185						190
Asn	Leu	Met	Glu	Ala	Phe	Arg	Arg	Asp	Leu	Asp	Ile	His	Thr	Lys	Thr
						195			200						205
Ala	Met	Asp	Ile	Phe	Gln	Val	Ser	Glu	Asp	Glu	Val	Thr	Pro	Asn	Met
						210			215						220
Arg	Arg	Gln	Ala	Lys	Ala	Val	Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile	Ser
225						230			235						240
Asp	Tyr	Gly	Leu	Ser	Gln	Asn	Leu	Gly	Ile	Ser	Arg	Lys	Glu	Ala	Ala
						245			250						255
Glu	Phe	Ile	Glu	Arg	Tyr	Phe	Glu	Ser	Phe	Pro	Gly	Val	Lys	Arg	Tyr
						260			265						270
Met	Glu	Asn	Ile	Val	Gln	Glu	Ala	Lys	Gln	Lys	Gly	Tyr	Val	Thr	Thr
						275			280						285
Leu	Leu	His	Arg	Arg	Arg	Tyr	Asp	Pro	Asp	Ile	Thr	Ser	Arg	Asn	Phe
						290			295						300
Asn	Val	Arg	Ser	Phe	Ala	Glu	Arg	Met	Ala	Met	Asn	Thr	Pro	Ile	Gln
305						310			315						320
Gly	Ser	Ala	Ala	Asp	Ile	Ile	Lys	Lys	Ala	Met	Ile	Asp	Leu	Asn	Ala
						325			330						335
Arg	Leu	Lys	Glu	Glu	Arg	Leu	Gln	Ala	Arg	Leu	Leu	Gln	Val	His	
						340			345						350
Asp	Glu	Leu	Ile	Leu	Glu	Ala	Pro	Lys	Glu	Glu	Met	Glu	Arg	Leu	Cys
						355			360						365
Arg	Leu	Val	Pro	Glu	Val	Met	Glu	Gln	Ala	Val	Thr	Leu	Arg	Val	Pro
						370			375						380
Leu	Lys	Val	Asp	Tyr	His	Tyr	Gly	Ser	Thr	Trp	Tyr	Asp	Ala	Lys	
						385			390						395

<210> SEQ ID NO 70

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 70

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Glu Gln Asp Glu Leu Leu Ile Lys Leu Glu Gln Pro Leu Ala Thr Ile
 1 5 10 15
 Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
 20 25 30
 Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Gly Ala Val Glu Gln
 35 40 45
 Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60
 Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80
 Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95
 Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110
 Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125
 Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln
 130 135 140
 Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160
 Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175
 Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190
 Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
 195 200 205
 Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
 210 215 220
 Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240
 Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
 245 250 255
 Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
 260 265 270
 Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285
 Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300
 Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320
 Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335
 Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
 340 345 350
 Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365
 Pro Lys Glu Glu Ile Glu Arg Leu Cys Arg Leu Val Pro Glu Val Met
 370 375 380
 Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400
 Gly Pro Thr Trp Tyr Asp Ala Lys
 405

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<210> SEQ_ID NO 71
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 71

Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu Ser Ser Ile
1           5          10          15

Leu Ala Glu Met Glu Phe Ala Gly Val Lys Val Asp Thr Lys Arg Leu
20          25          30

Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln
35          40          45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
50          55          60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
65          70          75          80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85          90          95

Ala Pro Tyr His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
100         105         110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115         120         125

Pro Asp Thr Lys Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
130         135         140

Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
145         150         155         160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165         170         175

Ser Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180         185         190

Val Leu Ala His Ile Ala Glu Asp Asp Asn Leu Met Glu Ala Phe Arg
195         200         205

Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe Gln Val
210         215         220

Ser Glu Asp Glu Val Thr Pro Asn Met Arg Arg Gln Ala Lys Ala Val
225         230         235         240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
245         250         255

Leu Asn Ile Ser Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260         265         270

Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
275         280         285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290         295         300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
305         310         315         320

Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325         330         335

Lys Lys Ala Met Ile Asp Leu Asn Ala Arg Leu Lys Glu Glu Arg Leu
340         345         350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
355         360         365

Pro Lys Glu Glu Met Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met

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370 375 380

Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400

Gly Ser Thr Trp Tyr Asp Ala Lys
 405

<210> SEQ ID NO 72
 <211> LENGTH: 408
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 72

Glu Gln Asp Glu Leu Leu Thr Lys Leu Glu Gln Pro Leu Ala Thr Ile
 1 5 10 15

Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
 20 25 30

Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala Val Glu Gln
 35 40 45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95

Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125

Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln
 130 135 140

Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160

Arg Leu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175

Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190

Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
 195 200 205

Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
 210 215 220

Ser Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
 245 250 255

Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
 260 265 270

Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile

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325	330	335	
Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu			
340	345	350	
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala			
355	360	365	
Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met			
370	375	380	
Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr			
385	390	395	400
Gly Pro Thr Trp Tyr Asp Ala Lys			
405			

<210> SEQ ID NO 73
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 73

Glu Gln Asp Glu Leu Phe Thr Asp Leu Glu Gln Pro Leu Ala Leu Ile			
1	5	10	15
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu			
20	25	30	
Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Ile Glu Gln			
35	40	45	
Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys			
50	55	60	
Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys			
65	70	75	80
Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu			
85	90	95	
Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu			
100	105	110	
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His			
115	120	125	
Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln			
130	135	140	
Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile			
145	150	155	160
Arg Leu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu			
165	170	175	
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg			
180	185	190	
Val Leu Ala His Ile Ala Asp Asp Glu Asn Leu Ile Glu Ala Phe Arg			
195	200	205	
Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val			
210	215	220	
Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val			
225	230	235	240
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn			
245	250	255	
Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe			
260	265	270	
Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile Val Gln Glu			

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275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335

Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
 340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365

Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met
 370 375 380

Glu Asn Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
 405

<210> SEQ ID NO 74

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 74

Glu Gln Asp Glu Leu Phe Thr Glu Leu Glu Leu Pro Leu Ala Leu Ile
 1 5 10 15

Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
 20 25 30

Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln
 35 40 45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95

Ala Pro His Arg Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125

Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
 130 135 140

Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175

Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190

Val Leu Ala His Ile Ala Asn Asp Asn Leu Ile Glu Ala Phe Arg
 195 200 205

Arg Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val Phe His Val
 210 215 220

Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala Lys Ala Val

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225	230	235	240
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn			
245	250	255	
Leu Gly Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe			
260	265	270	
Gln Ser Phe Pro Gly Val Lys Glu Tyr Met Glu Asp Ile Val Gln Glu			
275	280	285	
Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Phe			
290	295	300	
Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser Phe Ala Glu			
305	310	315	320
Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile			
325	330	335	
Lys Lys Ala Met Ile Asp Met Ala Ala Arg Leu Lys Glu Glu Arg Leu			
340	345	350	
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Phe Glu Ala			
355	360	365	
Pro Lys Glu Glu Ile Glu Arg Leu Glu Lys Leu Val Pro Glu Val Met			
370	375	380	
Glu His Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr Arg Tyr			
385	390	395	400
Gly Pro Thr Trp Tyr Asp Ala Lys			
405			

<210> SEQ ID NO 75

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 75

Glu	Gln	Asp	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Pro	Leu	Ile	Leu	Ile	
1			5			10								15	
Leu	Ala	Glu	Met	Glu	Phe	Thr	Gly	Val	Asp	Val	Asp	Thr	Lys	Arg	Leu
20			25												30
Glu	Gln	Met	Gly	Leu	Glu	Leu	Ala	Glu	Gln	Leu	Val	Glu	Gln	Glu	Gln
35			40												45
Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile	Asn	Ser	Pro	Lys
50				55											60
Gln	Leu	Gly	Leu	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu	Pro	Val	Leu	Lys
65				70											80
Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val	Leu	Glu	Lys	Leu
85				90											95
Ala	Pro	Glu	His	Glu	Ile	Val	Glu	Asn	Ile	Leu	His	Tyr	Arg	Gln	Leu
100				105											110
Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu	Gly	Leu	Leu	Lys	Val	Val	Asp
115				120											125
Thr	Asp	Thr	Gly	Lys	Val	His	Thr	Met	Phe	Asn	Gln	Ala	Leu	Thr	Gln
130				135											140
Thr	Gly	Arg	Leu	Ser	Ser	Ala	Glu	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Ile
145				150											160
Arg	Leu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	Val	Pro	Ser	Glu	
165				170											175
Pro	Leu	Trp	Leu	Ile	Phe	Ala	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg

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180	185	190
Val Leu Ala His Ile Ala Asp Asp Asn Leu Ala Glu Ala Phe Arg		
195	200	205
Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val		
210	215	220
Ser Glu Glu Glu Val Thr Ala Arg Met Arg Arg Gln Ala Lys Ala Val		
225	230	235
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn		
245	250	255
Leu Asn Ile Lys Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe		
260	265	270
Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Val Ile Val Gln Glu		
275	280	285
Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr		
290	295	300
Asp Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu		
305	310	315
Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile		
325	330	335
Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Gln Leu		
340	345	350
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala		
355	360	365
Pro Lys Glu Glu Met Glu Arg Leu Cys Val Leu Val Pro Glu Val Met		
370	375	380
Glu Gln Ala Val Arg Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr		
385	390	395
Gly Trp Thr Trp Tyr Asp Ala Lys		
405		

<210> SEQ_ID NO 76
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<400> SEQUENCE: 76

Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Leu Pro Leu Ala Leu Ile		
1	5	10
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu		
20	25	30
Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln		
35	40	45
Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys		
50	55	60
Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys		
65	70	75
Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu		
85	90	95
Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu		
100	105	110
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His		
115	120	125
Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln		

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130	135	140
Thr	Gly	Arg
Leu	Ser	Ser
Asp	Pro	Asn
Leu	Gln	Asn
Ile	Ile	Pro
145	150	155
160		
Arg	Leu	Glu
Glu	Gly	Arg
Lys	Ile	Arg
165	170	175
175		
Pro	Asp	Trp
Leu	Ile	Phe
Ala	Ala	Asp
Tyr	Ser	Gln
Ile	Glu	Ile
180	185	190
190		
Val	Leu	Ala
Ala	His	Ile
Ala	Asn	Asp
Asp	Asn	Leu
Ile	Glu	Ala
195	200	205
205		
Arg	Asp	Met
Asp	Ile	His
His	Thr	Lys
Thr	Ala	Met
Asp	Val	Phe
His	Val	
210	215	220
220		
Ser	Glu	Asp
Glu	Val	Thr
Ser	Asn	Met
Arg	Arg	Gln
Gln	Ala	Lys
Ala	Val	
225	230	235
235		
Asn	Phe	Gly
Ile	Val	Tyr
Gly	Ile	Ser
Asp	Tyr	Gly
Tyr	Gly	Leu
Leu	Ser	Gln
Asn		
245	250	255
255		
Leu	Gly	Ile
Ile	Thr	Arg
Arg	Glu	Ala
Ala	Ala	Glu
Phe	Ile	Glu
Glu	Arg	Tyr
Tyr	Phe	
260	265	270
270		
Glu	Ser	Phe
Phe	Pro	Gly
Gly	Val	Lys
Lys	Glu	Tyr
Tyr	Met	Glu
Glu	Asp	Ile
Ile	Val	Gln
Glu		
275	280	285
285		
Ala	Lys	Gln
Gln	Lys	Gly
Gly	Tyr	Val
Val	Thr	Thr
Thr	Leu	Leu
His	Arg	Arg
Arg	Arg	Tyr
290	295	300
300		
Leu	Pro	Glu
Ile	Thr	Ser
Ser	Arg	Asn
Asn	Phe	Asn
Leu	Arg	Ser
Arg	Phe	Ala
Ala	Glu	
305	310	315
315		
Arg	Thr	Ala
Ala	Met	Asn
Asn	Thr	Pro
Pro	Ile	Gln
Gly	Ser	Ala
Ala	Asp	Ile
Ile	Ile	
325	330	335
335		
Lys	Lys	Ala
Ala	Met	Ile
Ile	Asp	Met
Ala	Ala	Arg
Arg	Leu	Lys
Lys	Glu	Glu
Glu	Arg	Leu
Leu		
340	345	350
350		
Gln	Ala	Arg
Ala	Leu	Leu
Leu	Gln	Val
Gln	Val	His
His	Asp	Glu
Glu	Leu	Ile
Ile	Phe	Glu
Glu		
355	360	365
365		
Pro	Lys	Glu
Glu	Ile	Glu
Ile	Arg	Leu
Arg	Leu	Cys
Cys	Leu	Val
Leu	Val	Pro
Pro	Glu	Val
Glu		
370	375	380
380		
Glu	His	Ala
Ala	Val	Glu
Glu	Leu	Arg
Leu	Arg	Val
Arg	Val	Pro
Pro	Lys	Val
Lys	Val	Asp
Asp	Tyr	Tyr
Tyr	His	
His		
385	390	395
395		
Gly	Pro	Thr
Thr	Trp	Tyr
Tyr	Asp	Ala
Ala	Lys	
405		

<210> SEQ ID NO 77

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 77

Glu	Gln	Asp	Glu	Leu	Phe	Thr	Glu	Leu	Glu	Met	Pro	Leu	Ala	Leu	Ile
1				5			10			15					

Leu	Ala	Glu	Met	Glu	Phe	Thr	Gly	Val	Lys	Val	Asp	Thr	Lys	Arg	Leu
					20			25			30				

Glu	Gln	Met	Gly	Glu	Glu	Leu	Ala	Glu	Gln	Leu	Lys	Ala	Ile	Glu	Gln
					35			40			45				

Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile	Asn	Ser	Pro	Lys
					50			55			60				

Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu	Pro	Val	Leu	Lys
					65			70			75			80	

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu

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85	90	95
Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu		
100	105	110
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His		
115	120	125
Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln		
130	135	140
Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile		
145	150	155
Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu		
165	170	175
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg		
180	185	190
Val Leu Ala His Ile Ala Asn Asp Glu Asn Leu Ile Glu Ala Phe Arg		
195	200	205
Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val		
210	215	220
Ser Glu Asp Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val		
225	230	235
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn		
245	250	255
Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe		
260	265	270
Glu Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asp Ile Val Gln Glu		
275	280	285
Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr		
290	295	300
Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu		
305	310	315
Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile		
325	330	335
Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu		
340	345	350
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala		
355	360	365
Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met		
370	375	380
Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr		
385	390	395
Gly Pro Thr Trp Tyr Asp Ala Lys		
405		

<210> SEQ ID NO 78
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 78

Glu Gln Asp Glu Leu Leu Thr Lys Leu Glu Gln Pro Leu Ala Thr Ile		
1	5	10
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu		
20	25	30
Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Gly Ala Val Glu Gln		

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35	40	45
Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys		
50	55	60
Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys		
65	70	75
Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu		
85	90	95
Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu		
100	105	110
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His		
115	120	125
Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln		
130	135	140
Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile		
145	150	155
Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu		
165	170	175
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg		
180	185	190
Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg		
195	200	205
Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val		
210	215	220
Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val		
225	230	235
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn		
245	250	255
Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe		
260	265	270
Ala Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu		
275	280	285
Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr		
290	295	300
Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu		
305	310	315
Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile		
325	330	335
Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu		
340	345	350
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala		
355	360	365
Pro Lys Glu Glu Ile Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met		
370	375	380
Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr		
385	390	395
Gly Pro Thr Trp Tyr Asp Ala Lys		
405		

<210> SEQ ID NO 79

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 79

Glu Gln Asp Glu Leu Leu Ile Lys Leu Glu Leu Pro Leu Ala Thr Ile
 1 5 10 15
 Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
 20 25 30
 Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala Val Glu Gln
 35 40 45
 Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60
 Gln Leu Gly Ile Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80
 Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95
 Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110
 Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125
 Pro Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
 130 135 140
 Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160
 Arg Leu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175
 Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190
 Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
 195 200 205
 Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
 210 215 220
 Ser Glu Glu Val Thr Ala Arg Met Arg Arg Gln Ala Lys Ala Val
 225 230 235 240
 Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
 245 250 255
 Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
 260 265 270
 Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Thr Ile Val Gln Glu
 275 280 285
 Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300
 Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320
 Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335
 Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
 340 345 350
 Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365
 Pro Lys Glu Glu Met Glu Arg Leu Cys Gln Leu Val Pro Glu Val Met
 370 375 380
 Glu Gln Ala Val Ala Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400
 Gly Pro Thr Trp Tyr Asp Ala Lys
 405

-continued

<210> SEQ_ID NO 80
 <211> LENGTH: 408
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

 <400> SEQUENCE: 80

Glu	Gln	Asp	Glu	Leu	Leu	Thr	Glu	Leu	Glu	Gln	Pro	Leu	Ala	Leu	Ile	
1			5			10			15							
Leu	Ala	Glu	Met	Glu	Phe	Thr	Gly	Val	Lys	Val	Asp	Thr	Lys	Arg	Leu	
	20				25			30								
Glu	Gln	Met	Gly	Gly	Glu	Glu	Leu	Ala	Glu	Gln	Leu	Lys	Ala	Val	Glu	Gln
	35				40				45							
Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile	Asn	Ser	Pro	Lys	
	50				55			60								
Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu	Pro	Val	Leu	Lys	
	65				70			75		80						
Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val	Leu	Glu	Lys	Leu	
	85				90			95								
Ala	Pro	His	His	Glu	Ile	Val	Glu	Asn	Ile	Leu	His	Tyr	Arg	Gln	Leu	
	100				105			110								
Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu	Gly	Leu	Leu	Lys	Val	Val	His	
	115				120			125								
Pro	Asp	Thr	Gly	Lys	Val	His	Thr	Met	Phe	Asn	Gln	Ala	Leu	Thr	Gln	
	130				135			140								
Thr	Gly	Arg	Leu	Ser	Ser	Ala	Glu	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Ile	
	145				150			155		160						
Arg	Leu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	Val	Pro	Ser	Glu		
	165				170			175								
Pro	Asp	Trp	Leu	Ile	Phe	Ala	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	
	180				185			190								
Val	Leu	Ala	His	Ile	Ala	Asp	Asp	Asn	Leu	Ile	Glu	Ala	Phe	Arg		
	195				200			205								
Arg	Asp	Leu	Asp	Ile	His	Thr	Lys	Thr	Ala	Met	Asp	Ile	Phe	His	Val	
	210				215			220								
Ser	Glu	Glu	Glu	Val	Thr	Ala	Asn	Met	Arg	Arg	Gln	Ala	Lys	Ala	Val	
	225				230			235		240						
Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile	Ser	Asp	Tyr	Gly	Leu	Ala	Gln	Asn	
	245				250			255								
Leu	Asn	Ile	Thr	Arg	Lys	Glu	Ala	Ala	Glu	Phe	Ile	Glu	Arg	Tyr	Phe	
	260				265			270								
Ala	Ser	Phe	Pro	Gly	Val	Lys	Arg	Tyr	Met	Glu	Asp	Ile	Val	Gln	Glu	
	275				280			285								
Ala	Lys	Gln	Lys	Gly	Tyr	Val	Thr	Leu	Leu	His	Arg	Arg	Arg	Tyr		
	290				295			300								
Leu	Pro	Asp	Ile	Thr	Ser	Arg	Asn	Phe	Asn	Val	Arg	Ser	Phe	Ala	Glu	
	305				310			315		320						
Arg	Thr	Ala	Met	Asn	Thr	Pro	Ile	Gln	Gly	Ser	Ala	Ala	Asp	Ile	Ile	
	325				330			335								
Lys	Lys	Ala	Met	Ile	Asp	Leu	Ala	Ala	Arg	Leu	Lys	Glu	Glu	Arg	Leu	
	340				345			350								
Gln	Ala	Arg	Leu	Leu	Leu	Gln	Val	His	Asp	Glu	Leu	Ile	Leu	Glu	Ala	
	355				360			365								

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Pro Lys Glu Glu Ile Glu Arg Leu Cys Lys Leu Val Pro Glu Val Met
370 375 380

Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ ID NO 81

<211> LENGTH: 408

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 81

Glu Gln Tyr Glu Leu Phe Thr Asp Leu Glu Met Pro Leu Ala Leu Ile
1 5 10 15

Leu Ala Asp Met Glu Tyr Thr Gly Val Lys Val Asp Val Glu Arg Leu
20 25 30

Lys Glu Met Gly Glu Glu Leu Ala Glu Arg Leu Lys Glu Ile Glu Gln
35 40 45

Lys Ile Tyr Glu Leu Ala Gly Glu Glu Phe Asn Ile Asn Ser Pro Lys
50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gly Leu Pro Val Ile Lys
65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95

Ala Ser Lys His Glu Ile Ile Arg Asn Ile Leu His Tyr Arg Gln Leu
100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115 120 125

Gln Asp Thr Gly Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
130 135 140

Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Ile
145 150 155 160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165 170 175

Glu Gly Trp Val Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180 185 190

Val Leu Ala His Ile Ala Asn Asp Glu Lys Leu Ile Glu Ala Phe Arg
195 200 205

His Asp Met Asp Ile His Thr Lys Thr Ala Met Asp Val Phe His Val
210 215 220

Ser Glu Asp Glu Val Thr Ser Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn
245 250 255

Leu Gly Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Leu
260 265 270

Glu Ser Phe Pro Gly Val Lys Glu Tyr Met Asp Asp Ile Val Gln Glu
275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Leu Pro Glu Ile Thr Ser Arg Asn Phe Asn Leu Arg Ser Phe Ala Glu
305 310 315 320

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Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335
Lys Lys Ala Met Ile Asp Met Ala Asn Arg Leu Lys Glu Glu Asn Leu
340 345 350
Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Phe Glu Ala
355 360 365
Pro Lys Glu Glu Ile Glu Lys Leu Lys Ile Val Pro Glu Val Met
370 375 380
Glu His Ala Val Glu Leu Lys Val Pro Leu Lys Val Asp Tyr Ser Tyr
385 390 395 400
Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ ID NO: 82
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 82

Glu Gln Asp Glu Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Ala Ile
1 5 10 15
Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
20 25 30
Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Lys Glu Val Glu Gln
35 40 45
Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
50 55 60
Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
65 70 75 80
Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95
Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
100 105 110
Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115 120 125
Pro Asp Thr Lys Lys Val His Thr Arg Phe Asn Gln Ala Leu Thr Gln
130 135 140
Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
145 150 155 160
Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165 170 175
Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180 185 190
Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
195 200 205
Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
210 215 220
Ser Glu Asp Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240
Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn
245 250 255
Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260 265 270

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Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu Asn Ile Val Gln Glu
 275 280 285
 Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
 290 295 300
 Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
 305 310 315 320
 Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
 325 330 335
 Lys Lys Ala Met Ile Asp Leu Ala Lys Arg Leu Lys Glu Glu Arg Leu
 340 345 350
 Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
 355 360 365
 Pro Lys Glu Glu Ile Glu Arg Leu Glu Lys Leu Val Pro Glu Val Met
 370 375 380
 Glu Gln Ala Val Glu Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
 385 390 395 400
 Gly Pro Thr Trp Tyr Asp Ala Lys
 405

<210> SEQ_ID NO 83
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<400> SEQUENCE: 83

Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Ser Ile
 1 5 10 15
 Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
 20 25 30
 Glu Gln Met Gly Glu Glu Leu Thr Glu Gln Leu Arg Ala Val Glu Gln
 35 40 45
 Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
 50 55 60
 Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
 65 70 75 80
 Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
 85 90 95
 Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
 100 105 110
 Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
 115 120 125
 Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln
 130 135 140
 Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
 145 150 155 160
 Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
 165 170 175
 Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
 180 185 190
 Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
 195 200 205
 Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
 210 215 220

-continued

Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
245 250 255

Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260 265 270

Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile Val Gln Glu
275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
305 310 315 320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335

Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Arg Leu
340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
355 360 365

Pro Lys Glu Glu Ile Glu Arg Leu Cys Arg Leu Val Pro Glu Val Met
370 375 380

Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ ID NO 84
<211> LENGTH: 408
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 84

Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro Leu Ala Ser Ile
1 5 10 15

Leu Ala Glu Met Glu Phe Thr Gly Val Lys Val Asp Thr Lys Arg Leu
20 25 30

Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Arg Ala Val Glu Gln
35 40 45

Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser Pro Lys
50 55 60

Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val Leu Lys
65 70 75 80

Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu Glu Lys Leu
85 90 95

Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr Arg Gln Leu
100 105 110

Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys Val Val His
115 120 125

Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala Leu Thr Gln
130 135 140

Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile
145 150 155 160

Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ser Glu
165 170 175

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Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg
180 185 190

Val Leu Ala His Ile Ala Asp Asp Asn Leu Ile Glu Ala Phe Arg
195 200 205

Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile Phe His Val
210 215 220

Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala Lys Ala Val
225 230 235 240

Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ala Gln Asn
245 250 255

Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu Arg Tyr Phe
260 265 270

Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile Val Gln Glu
275 280 285

Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg Arg Arg Tyr
290 295 300

Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser Phe Ala Glu
305 310 315 320

Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile
325 330 335

Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu Glu Arg Leu
340 345 350

Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile Leu Glu Ala
355 360 365

Pro Lys Glu Glu Ile Glu Arg Leu Cys Arg Leu Val Pro Glu Val Met
370 375 380

Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp Tyr His Tyr
385 390 395 400

Gly Pro Thr Trp Tyr Asp Ala Lys
405

<210> SEQ_ID NO 85
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 85

Glu Glu Glu Lys Pro Leu Glu Asp Ile Glu Phe Ala Ile Ala Asp
1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Asn
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Ser Pro Gln Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Thr Ala Glu Asp Ile Ala Ala Val Ala Lys Met Lys
115 120 125

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Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Val
 130 135 140

Lys Arg Ser Leu Pro Asp Glu Gln Ala Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Asp Leu
 165 170 175

Arg Lys Asn

<210> SEQ ID NO 86

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 86

Ala Glu Glu Glu Lys Pro Leu Glu Glu Met Glu Phe Thr Asp Val Asp
 1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Gln Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60

Asp Pro Gln Phe Val Ala Trp Leu Glu Asp Glu Thr Lys Lys Ser
 65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asn Pro Ala Gln Asp Asp Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Ala
 130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Arg Ala Leu Glu Gln Pro Phe Ile Asp Glu Leu
 165 170 175

Arg Arg Arg

<210> SEQ ID NO 87

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 87

Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Thr Ile Ala Asp
 1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

Val Asn Glu Arg Gly Arg Phe Phe Leu Arg Thr Glu Thr Ala Leu Ala
 50 55 60

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Asp	Pro	Gln	Phe	Lys	Ala	Trp	Leu	Ala	Asp	Glu	Thr	Lys	Lys	Lys	Ser
65															80

Met	Phe	Asp	Ala	Lys	Arg	Ala	Ile	Val	Ala	Leu	Lys	Trp	Lys	Gly	Ile
															95

Glu	Leu	Arg	Gly	Val	Asp	Phe	Asp	Leu	Leu	Leu	Ala	Ala	Tyr	Leu	Leu

Asn	Pro	Ala	Gln	Asp	Ala	Gly	Asp	Val	Ala	Ala	Val	Ala	Lys	Met	Lys
															125

Gln	Tyr	Glu	Ala	Val	Arg	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Ala

Lys	Arg	Ala	Leu	Pro	Asp	Glu	Pro	Thr	Leu	Ala	Glu	His	Leu	Val	Arg
145															160

Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Glu	Pro	Phe	Leu	Asp	Glu	Leu

Arg Glu Asn

<210> SEQ_ID NO 88

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 88

Ala	Glu	Glu	Glu	Pro	Leu	Ala	Asp	Met	Glu	Phe	Ala	Ile	Ala	Asp	
1															15

Glu	Val	Thr	Glu	Glu	Met	Leu	Ala	Asp	Lys	Ala	Ala	Leu	Val	Val	Glu
															30

Val	Met	Glu	Asp	Asn	Tyr	His	Asp	Ala	Pro	Ile	Val	Gly	Phe	Ala	Asn
															45

Val	Asn	Glu	His	Gly	Arg	Phe	Phe	Leu	Arg	Ala	Glu	Leu	Ala	Leu	Ala
															60

Asp	Ser	Gln	Phe	Leu	Ala	Trp	Leu	Glu	Asp	Glu	Thr	Lys	Lys	Ser	
65															80

Met	Phe	Asp	Arg	Lys	Arg	Ala	Ala	Val	Ala	Leu	Lys	Trp	Lys	Gly	Ile
															95

Glu	Leu	Arg	Gly	Val	Ala	Phe	Asp	Leu	Leu	Ala	Ala	Tyr	Leu	Leu	
															110

Asn	Pro	Ala	Gln	Asp	Ala	Asp	Asp	Val	Ala	Ala	Val	Ala	Lys	Met	Lys
															125

Gln	Tyr	Glu	Ala	Val	Arg	Pro	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Ala
															140

Lys	Arg	Ser	Val	Pro	Asp	Glu	Pro	Val	Leu	Ala	Glu	His	Leu	Val	Arg
145															160

Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Arg	Pro	Phe	Leu	Asp	Glu	Leu
															175

Arg Arg Asn

<210> SEQ_ID NO 89

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 89

Ala Glu Gly Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Val Asp

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1	5	10	15
Glu	Ile	Thr	Glu
Glu	Glu	Met	Leu
Met	Ala	Asp	Lys
Ala	Ala	Ala	Leu
Leu	Val	Val	Glu
20	25	30	
Val	Met	Glu	Glu
Glu	Asn	Tyr	His
Asp	Ala	Pro	Ile
Ile	Val	Gly	Ile
35	40	45	Ala
Leu			Leu
Val	Asn	Glu	His
Gly	Arg	Phe	Phe
Phe	Leu	Arg	Pro
Leu	Ala	Glu	Thr
Ala	Trp	Thr	Ala
Trp	Leu	Lys	Leu
Leu	Ala	Lys	Ala
Asp	Pro	Gln	Phe
Phe	Leu	Ala	Asp
Leu	Ala	Trp	Glu
Ala	Asp	Leu	Thr
Asp	Glu	Ala	Lys
Glu	Thr	Ala	Arg
Arg	Asp	Ala	Gly
Gly	Asp	Val	Asp
Asp	Leu	Leu	Leu
Leu	Ala	Ala	Tyr
Ala	Tyr	Leu	Leu
Asn	Pro	Ala	Gln
Gln	Asp	Ala	Gly
Ala	Gly	Asp	Val
Asp	Val	Ala	Ala
Val	Ala	Val	Lys
Lys	Met	Val	Met
Met	Asp	Ala	Lys
Ala	Lys	Ala	Met
Leu	Asn	Val	Lys
Asn	Pro	Ala	Asp
Pro	Ala	Asp	Asp
Ala	Asp	Val	Ala
Asp	Val	Ala	Ala
Val	Ala	Val	Lys
Lys	Met	Val	Met
Met	Asp	Ala	Lys
Ala	Lys	Val	Asn
Asn	Arg	Ala	Asn

<210> SEQ_ID NO 90

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 90

1	5	10	15
Ala	Glu	Glu	Lys
Pro	Leu	Glu	Asp
Ile	Glu	Phe	Asp
Ile	Asp	Ile	Asp
1	5	10	15
Glu	Val	Thr	Glu
Glu	Met	Leu	Ala
Met	Asp	Lys	Ala
Ala	Ala	Leu	Val
Leu	Val	Val	Glu
20	25	30	
Val	Gln	Glu	Asp
Asn	Tyr	His	Asp
Ala	Pro	Ile	Val
Pro	Ile	Gly	Phe
Ile	Val	Ala	Ile
35	40	45	
Val	Asn	Glu	His
Gly	Arg	Phe	Phe
Phe	Ile	Arg	Thr
Ile	Arg	Thr	Ala
50	55	60	
Ser	Pro	Gln	Phe
Phe	Lys	Ala	Trp
Lys	Ala	Asp	Glu
Ala	Asp	Thr	lys
Asp	Glu	lys	Ser
Glu	lys	lys	80
Ser	Pro	Gln	Phe
Phe	Asp	Ala	Lys
Asp	Ala	Lys	Arg
Ala	Lys	Arg	Ala
Leu	Val	Ala	Ile
Ile	Val	Ala	Leu
85	90	95	
Glu	Leu	Arg	Gly
Gly	Val	Asp	Phe
Phe	Asp	Leu	Leu
Asp	Leu	Leu	Ala
Leu	Ala	Ala	Tyr
100	105	110	Leu
Asn	Pro	Ala	Gln
Gln	Thr	Ala	Asp
Asp	Asp	Val	Ala
Val	Ala	Ala	Lys
Lys	Met	Val	Met
Met	Asp	Ala	Lys
Ala	Lys	Val	Asn
Asn	Arg	Ala	Asn

Arg Lys Asn

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<210> SEQ ID NO 91
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 91

Glu	Glu	Glu	Glu	Lys	Pro	Leu	Glu	Asp	Ile	Ser	Phe	Glu	Ile	Ala	Asp
1				5			10					15			
Glu	Val	Thr	Glu	Asp	Met	Leu	Thr	Asp	Glu	Ser	Ala	Leu	Val	Val	Glu
	20				25							30			
Val	Leu	Glu	Glu	Asn	Tyr	His	Lys	Ala	Asp	Ile	Val	Gly	Phe	Ala	Ile
	35					40						45			
Ala	Asn	Glu	Asn	Gly	Asn	Phe	Phe	Ile	Pro	Thr	Asp	Thr	Ala	Leu	Ala
	50					55						60			
Ser	Pro	Gln	Phe	Lys	Lys	Trp	Leu	Glu	Asp	Glu	Thr	Lys	Lys	Ser	
	65					70						80			
Val	Phe	Asp	Ala	Lys	Arg	Ala	Ile	Val	Ala	Leu	Lys	Trp	His	Gly	Ile
	85						90					95			
Glu	Leu	Lys	Gly	Val	Asp	Phe	Asp	Leu	Leu	Ile	Ala	Ser	Tyr	Leu	Leu
	100					105						110			
Asn	Pro	Ser	Glu	Ser	Ser	Asp	Asp	Phe	Ala	Ser	Val	Ala	Lys	Thr	Lys
	115					120						125			
Gly	Tyr	Asn	Ala	Val	Gln	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Ala
	130					135						140			
Lys	Arg	Ala	Val	Pro	Asp	Glu	Glu	Lys	Leu	Ala	Glu	His	Leu	Ala	Arg
	145					150						155			160
Lys	Ala	Ala	Ala	Ile	Ser	Ala	Leu	Lys	Glu	Thr	Phe	Ile	His	Glu	Leu
	165					170						175			
Lys	Glu	Asn													

<210> SEQ ID NO 92
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 92

Thr	Glu	Glu	Glu	Glu	Leu	Glu	Asp	Ile	Asn	Val	Lys	Thr	Ala	Asp	
1					5		10				15				
Glu	Val	Thr	Ser	Glu	Met	Leu	Thr	Asp	Pro	Ser	Ala	Leu	Val	Val	Glu
	20				25							30			
Gln	Leu	Gly	Asp	Asn	Tyr	His	Glu	Ala	Asp	Ile	Ile	Gly	Phe	Ala	Ile
	35					40						45			
Val	Asn	Glu	Asn	Gly	Ala	Phe	Phe	Ile	Pro	Lys	Glu	Thr	Ala	Leu	Gln
	50					55						60			
Ser	Pro	Gln	Phe	Lys	Glu	Trp	Val	Glu	Asp	Glu	Thr	Lys	Lys	Trp	
	65					70						80			
Val	Phe	Asp	Ser	Lys	Arg	Ala	Ile	Val	Ala	Leu	Arg	Trp	His	Gly	Ile
	85						90					95			
Glu	Leu	Lys	Gly	Val	Asp	Phe	Asp	Val	Leu	Leu	Ala	Ser	Tyr	Ile	Ile
	100					105						110			
Asn	Pro	Ser	Asn	Ser	Tyr	Asp	Asp	Val	Ala	Ser	Val	Ala	Lys	Glu	Tyr
	115					120						125			

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Gly Leu Asn Ile Val Ser Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Ala Glu Asp Glu Leu Ala Glu His Leu Gly Arg
145 150 155 160

Lys Ala Ala Ala Ile Ser Ala Leu Arg Asp Lys Leu Leu Gln Ala Leu
165 170 175

Glu Glu Asn

<210> SEQ ID NO 93

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 93

Ala Glu Glu Glu Val Pro Leu Ala Glu Met Glu Phe Val Ile Ala Asp
1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Ala
130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Arg Asn

<210> SEQ ID NO 94

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 94

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Val Ile Ala Asp
1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Ser Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser

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65	70	75	80
Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile			
85	90	95	
Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu			
100	105	110	
Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys			
115	120	125	
Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala			
130	135	140	
Lys Arg Ala Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg			
145	150	155	160
Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu			
165	170	175	
Arg Arg Asn			

<210> SEQ ID NO 95
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 95

Glu Glu Glu Glu Val Pro Leu Glu Glu Ile Glu Phe Ala Ile Ala Asp			
1	5	10	15
Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu			
20	25	30	
Val Leu Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Phe Ala Leu			
35	40	45	
Val Asn Glu His Gly Arg Phe Phe Ile Arg Pro Glu Thr Ala Leu Ala			
50	55	60	
Ser Ser Gln Phe Lys Ala Trp Leu Glu Asp Glu Thr Lys Lys Ser			
65	70	75	80
Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile			
85	90	95	
Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Ala Ala Tyr Leu Leu			
100	105	110	
Asn Pro Ala Gln Ser Ala Glu Asp Val Ala Ala Val Ala Lys Met Lys			
115	120	125	
Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala			
130	135	140	
Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg			
145	150	155	160
Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Ile Asp Glu Leu			
165	170	175	
Arg Glu Asn			

<210> SEQ ID NO 96
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 96

Ala Glu Glu Glu Ala Pro Leu Glu Asp Ile Glu Phe Asp Ile Ala Asp			
1	5	10	15

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Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Gln Glu Asp Asn Tyr His Asp Ala Pro Ile Val Gly Phe Ala Ile
 35 40 45

Val Asn Glu Arg Gly Arg Phe Phe Ile Arg Thr Glu Thr Ala Leu Ala
 50 55 60

Ser Glu Ala Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80

Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asn Pro Ala Gln Thr Ala Asp Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

Gln Tyr His Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Leu Asp Glu Leu
 165 170 175

Arg Lys Asn

<210> SEQ ID NO 97
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<400> SEQUENCE: 97

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp
 1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Val Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60

Ser Pro Gln Phe Leu Ala Trp Leu Gly Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80

Met Phe Asp Ser Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asn Pro Ala Gln Ala Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

Lys Arg Ser Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Glu Leu
 165 170 175

Arg Arg Asn

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<210> SEQ_ID NO 98
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 98

Ala	Glu	Glu	Glu	Lys	Pro	Leu	Ala	Glu	Met	Glu	Phe	Val	Ile	Ala	Asp
1									5				10		15

Glu Ile Thr Asp Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Ser Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Arg Asn

<210> SEQ_ID NO 99
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 99

Ala	Glu	Glu	Glu	Lys	Pro	Leu	Glu	Glu	Met	Glu	Phe	Ala	Ile	Ala	Asp
1									5				10		15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Ser Pro Gln Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Gly Ala

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130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
 165 170 175

Arg Asn Asn

<210> SEQ ID NO 100

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 100

Ala Glu Glu Glu Val Pro Leu Glu Glu Met Glu Phe Thr Ile Ala Asp
 1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Leu Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60

Asp Pro Gln Phe Val Ala Trp Leu Glu Asp Glu Thr Lys Lys Ser
 65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Ala
 130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
 165 170 175

Arg Glu Asn

<210> SEQ ID NO 101

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 101

Ala Glu Glu Glu Val Pro Leu Glu Glu Met Glu Phe Val Ile Ala Asp
 1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Ala Glu Thr Ala Leu Ala
 50 55 60

Asp Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
 65 70 75 80

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Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Glu Asn

<210> SEQ ID NO 102

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 102

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Val Ile Ala Asp
1 5 10 15

Gly Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Arg Asn

<210> SEQ ID NO 103

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 103

Ala Glu Glu Glu Lys Pro Leu Glu Glu Met Glu Phe Ala Ile Ala Asp
1 5 10 15

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Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Met Arg Pro Glu Thr Ala Leu Ala
50 55 60

Ser Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Ile Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Val
130 135 140

Lys Arg Ser Leu Pro Asp Glu Gln Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Asp Leu
165 170 175

Arg Asn Asn

<210> SEQ ID NO 104

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 104

Glu Glu Glu Lys Pro Leu Glu Asp Ile Ser Phe Glu Ile Ala Asp
1 5 10 15

Glu Val Thr Glu Glu Met Leu Thr Asp Glu Ser Ala Leu Val Val Glu
20 25 30

Val Leu Glu Glu Asn Tyr His Lys Ala Asp Ile Val Gly Phe Ala Ile
35 40 45

Val Asn Glu Asn Gly Asn Phe Phe Ile Pro Thr Asp Thr Ala Leu Ala
50 55 60

Ser Pro Gln Phe Lys Lys Trp Leu Glu Asp Glu Thr Lys Lys Thr
65 70 75 80

Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Lys Gly Val Asp Phe Asp Leu Leu Ile Ala Ser Tyr Leu Leu
100 105 110

Asn Pro Ser Glu Thr Asn Asp Asp Phe Ala Ser Val Ala Lys Thr Lys
115 120 125

Gly Tyr Asn Ala Val Gln Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Glu Glu Lys Leu Ala Glu His Leu Ala Arg
145 150 155 160

Lys Ala Ala Ala Ile Ser Ala Leu Lys Glu Thr Phe Ile Gln Glu Leu
165 170 175

Lys Glu Asn

<210> SEQ ID NO 105

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<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 105

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp
1           5          10          15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20          25          30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35          40          45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50          55          60

Asp Ser Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
65          70          75          80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85          90          95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
100         105         110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115         120         125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130         135         140

Lys Arg Ser Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145         150         155         160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Leu Asp Glu Leu
165         170         175

Arg Arg Asn

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<210> SEQ ID NO 106
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 106

Glu Glu Glu Glu Lys Pro Leu Ala Lys Ile Ala Phe Thr Leu Ala Asp
1           5          10          15

Arg Val Thr Asp Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20          25          30

Val Val Glu Asp Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Val
35          40          45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50          55          60

Asp Pro Gln Phe Val Ala Trp Leu Gly Asp Glu Thr Lys Lys Lys Ser
65          70          75          80

Val Phe Asp Ser Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85          90          95

Glu Leu Cys Gly Val Ser Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100         105         110

Asp Pro Ala Gln Gly Val Asp Asp Val Ala Ala Ala Lys Met Lys
115         120         125

Gln Tyr His Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala
130         135         140

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Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
 165 170 175

Arg Arg Asn

<210> SEQ ID NO 107

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 107

Ala Glu Asp Glu Lys Pro Leu Glu Glu Ile Glu Phe Ala Ile Ala Asp
 1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Leu Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Phe Ala Ile
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Ile Arg Pro Glu Thr Ala Leu Ala
 50 55 60

Ser Ser Gln Phe Lys Ala Trp Leu Glu Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asn Pro Ala Gln Ser Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Leu Asp Glu Leu
 165 170 175

Arg Glu Asn

<210> SEQ ID NO 108

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 108

Ala Glu Glu Ala Pro Leu Glu Asp Ile Glu Phe Asp Ile Ala Asp
 1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Gln Glu Asp Asn Tyr His Asp Ala Pro Ile Val Gly Phe Ala Ile
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Ile Arg Thr Glu Thr Ala Leu Ala
 50 55 60

Ser Glu Ala Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80

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Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Thr Ala Asp Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr His Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Leu Asp Glu Leu
165 170 175

Arg Lys Asn

<210> SEQ ID NO 109

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 109

Ala Glu Asp Glu Lys Pro Leu Ala Glu Met Glu Phe Val Ile Ala Asp
1 5 10 15

Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Arg Asn

<210> SEQ ID NO 110

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 110

Thr Glu Glu Glu Val Glu Asp Ile Asn Val Lys Thr Val Thr
1 5 10 15

Glu Val Thr Ser Glu Met Leu Thr Asp Pro Ser Ala Leu Val Val Glu

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20

25

30

Gln Leu Gly Asp Asn Tyr His Glu Ala Asp Ile Ile Gly Phe Ala Ile
35 40 45

Val Asn Glu Asn Gly Ala Phe Phe Ile Pro Lys Glu Thr Ala Leu Gln
50 55 60

Ser Glu Ala Phe Lys Glu Trp Val Glu Asp Glu Thr Lys Lys Lys Trp
65 70 75 80

Val Phe Asp Ser Lys Arg Ala Val Val Ala Leu Arg Trp His Gly Ile
85 90 95

Glu Leu Lys Gly Val Asp Phe Asp Val Leu Leu Ala Ser Tyr Ile Ile
100 105 110

Asn Pro Ser Asn Ser Tyr Asp Asp Val Ala Ser Val Ala Lys Glu Tyr
115 120 125

Gly Leu Asn Ile Val Ser Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Ala Glu Asp Glu Leu Ala Glu His Leu Gly Arg
145 150 155 160

Lys Ala Ala Ala Ile Ser Ala Leu Arg Asp Lys Leu Leu Gln Ala Leu
165 170 175

Glu Glu Asn

<210> SEQ ID NO 111

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 111

Ala Glu Lys Glu Leu Pro Leu Met Glu Met Glu Phe Ala Asp Ala Asp
1 5 10 15

Thr Ile Thr Met Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Asn
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Thr Glu Leu Ala Leu Ala
50 55 60

Asp Phe Gln Phe Val Ala Trp Leu Glu Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Arg Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Val Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Ala Pro Ala Gln Asp Asp Gly Asp Ala Ala Ala Lys Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Glu Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Pro Asp Pro Asp Glu Leu Ala Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Glu Asn

<210> SEQ ID NO 112

<211> LENGTH: 179

-continued

<212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

 <400> SEQUENCE: 112

 Ala Glu Asp Glu Thr Pro Leu Met Glu Met Glu Phe Val Ile Ala Asp
 1 5 10 15

 Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

 Val Gln Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

 Val Asn Glu His Gly Arg Phe Phe Leu Arg Ala Glu Met Ala Leu Ala
 50 55 60

 Asp Pro Gln Phe Val Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80

 Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

 Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

 Asn Pro Ala Gln Thr Asp Glu Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

 Gln Tyr Glu Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

 Lys Arg Pro Leu Pro Asp Glu Pro Ala Leu Ala Glu His Leu Val Arg
 145 150 155 160

 Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
 165 170 175

 Arg Ser Asn

<210> SEQ_ID NO 113
 <211> LENGTH: 179
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

 <400> SEQUENCE: 113

 Ala Glu Glu Glu Lys Pro Leu Glu Asp Ile Glu Phe Glu Ile Ala Asp
 1 5 10 15

 Glu Val Thr Glu Glu Met Leu Ala Asp Glu Ala Ala Leu Val Val Glu
 20 25 30

 Val Leu Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Phe Ala Leu
 35 40 45

 Val Asn Glu His Gly Arg Phe Phe Ile Arg Thr Glu Thr Ala Leu Ala
 50 55 60

 Ser Ser Gln Phe Lys Ala Trp Leu Glu Asp Glu Thr Lys Lys Lys Ser
 65 70 75 80

 Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

 Glu Leu Arg Gly Val Asp Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

 Asn Pro Ala Gln Ser Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

 Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

-continued

Lys Arg Ala Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Ile Asp Glu Leu
 165 170 175

Arg Glu Asn

<210> SEQ ID NO 114

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 114

Ser Glu Glu Glu Lys Pro Leu Ala Lys Met Ala Phe Thr Leu Ala Asp
 1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Val Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Val
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60

Ser Pro Gln Phe Val Ala Trp Leu Gly Asp Glu Thr Lys Lys Ser
 65 70 75 80

Met Phe Asp Ser Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
 85 90 95

Glu Leu Cys Gly Val Ser Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asp Pro Ala Gln Gly Val Asp Asp Val Ala Ala Ala Lys Met Lys
 115 120 125

Gln Tyr Glu Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
 165 170 175

Arg Arg Asn

<210> SEQ ID NO 115

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 115

Ala Glu Gly Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Val Asp
 1 5 10 15

Glu Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
 20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
 35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
 50 55 60

Asp Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
 65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile

-continued

85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Ile Asp Glu Leu
165 170 175

Arg Arg Asn

<210> SEQ ID NO 116

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 116

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Thr Ile Ala Asp
1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Leu Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Ser Gln Phe Leu Ala Trp Leu Glu Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Ala Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Ile Asp Glu Leu
165 170 175

Arg Arg Asn

<210> SEQ ID NO 117

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 117

Ala Glu Glu Glu Lys Pro Leu Glu Glu Met Glu Phe Ala Ile Ala Asp
1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

-continued

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Ser Pro Gln Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Asn Asn

<210> SEQ ID NO 118

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 118

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp
1 5 10 15

Ser Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Val Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Leu Ala Trp Leu Gly Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ser Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Glu Leu
165 170 175

Arg Arg Asn

<210> SEQ ID NO 119

<211> LENGTH: 179

<212> TYPE: PRT

-continued

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 119

Ala	Glu	Glu	Glu	Lys	Pro	Leu	Ala	Glu	Met	Glu	Phe	Ala	Ile	Ala	Asp
1									5	10				15	

Glu	Ile	Thr	Glu	Glu	Met	Leu	Ala	Asp	Lys	Ala	Ala	Leu	Val	Val	Glu
									20	25			30		

Val	Met	Glu	Glu	Asn	Tyr	His	Asp	Ala	Pro	Ile	Val	Gly	Ile	Ala	Leu
										35	40		45		

Val	Asn	Glu	His	Gly	Arg	Phe	Phe	Leu	Arg	Thr	Glu	Thr	Ala	Leu	Ala
									50	55		60			

Asp	Pro	Gln	Phe	Lys	Ala	Trp	Leu	Ala	Asp	Glu	Thr	Lys	Lys	Ser
65									70	75		80		

Met	Phe	Asp	Ala	Lys	Arg	Ala	Ile	Val	Ala	Leu	Lys	Trp	Lys	Gly	Ile
								85	90		95				

Glu	Leu	Arg	Gly	Val	Asp	Phe	Asp	Leu	Leu	Leu	Ala	Tyr	Leu	Leu
								100	105		110			

Asn	Pro	Ala	Gln	Asp	Ala	Gly	Asp	Val	Ala	Ala	Val	Ala	Lys	Met	Lys
								115	120		125				

Gln	Tyr	Glu	Ala	Val	Arg	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Ala
								130	135		140				

Lys	Arg	Ala	Leu	Pro	Asp	Glu	Pro	Thr	Leu	Ala	Glu	His	Leu	Val	Arg
145								150	155		160				

Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Glu	Pro	Phe	Leu	Asp	Glu	Leu
								165	170		175				

Arg Glu Asn

<210> SEQ ID NO 120

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 120

Ser	Glu	Glu	Glu	Pro	Leu	Ala	Lys	Ile	Ala	Phe	Asp	Leu	Ala	Asp
1								5	10		15			

Arg	Val	Thr	Glu	Glu	Met	Leu	Ala	Asp	Lys	Ala	Ala	Leu	Val	Val	Glu
								20	25		30				

Val	Gln	Glu	Asp	Asn	Tyr	His	Asp	Ala	Pro	Ile	Val	Gly	Ile	Ala	Val
								35	40		45				

Val	Asn	Glu	His	Gly	Arg	Phe	Phe	Leu	Arg	Ala	Glu	Leu	Ala	Leu	Ala
								50	55		60				

Ser	Pro	Gln	Phe	Val	Ala	Trp	Leu	Gly	Asp	Glu	Thr	Lys	Lys	Ser
65								70	75		80			

Met	Phe	Asp	Ser	Lys	Arg	Ala	Ile	Val	Ala	Leu	Lys	Trp	Lys	Gly	Ile
								85	90		95				

Glu	Leu	Cys	Gly	Val	Asp	Phe	Asp	Leu	Leu	Leu	Ala	Tyr	Leu	Leu
								100	105		110			

Asp	Pro	Ala	Gln	Thr	Asp	Asp	Ala	Ala	Ala	Lys	Ala	Lys	Met	Lys
								115	120		125			

Gln	Tyr	His	Ala	Val	Arg	Pro	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Ala
								130	135		140				

Lys	Arg	Ala	Val	Pro	Asp	Glu	Pro	Val	Leu	Ala	Glu	His	Leu	Val	Arg
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-continued

145	150	155	160
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Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Phe Leu Asp Glu Leu	165	170	175
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Arg Arg Asn

<210> SEQ ID NO 121

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 121

Ala Glu Asp Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp	5	10	15
---	---	----	----

Gly Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu	20	25	30
---	----	----	----

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu	35	40	45
---	----	----	----

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala	50	55	60
---	----	----	----

Asp Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser	65	70	75
---	----	----	----

80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile	85	90	95
---	----	----	----

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu	100	105	110
---	-----	-----	-----

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys	115	120	125
---	-----	-----	-----

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala	130	135	140
---	-----	-----	-----

Lys Arg Ser Leu Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg	145	150	155
---	-----	-----	-----

160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Glu Leu	165	170	175
---	-----	-----	-----

Arg Ser Asn

<210> SEQ ID NO 122

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 122

Ala Glu Glu Glu Lys Pro Leu Glu Glu Met Glu Phe Ala Ile Ala Asp	5	10	15
---	---	----	----

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu	20	25	30
---	----	----	----

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu	35	40	45
---	----	----	----

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala	50	55	60
---	----	----	----

Asp Pro Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser	65	70	75
---	----	----	----

80

Met Phe Asp Ala Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile	85	90	95
---	----	----	----

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Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
 100 105 110

Asn Pro Ala Gln Asp Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
 115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
 145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
 165 170 175

Arg Arg Asn

<210> SEQ_ID NO 123

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 123

Glu Glu Glu Glu Glu Pro Leu Glu Asp Ile Ser Phe Glu Ile Val Glu
 1 5 10 15

Glu Val Thr Glu Asp Met Leu Thr Asp Glu Ser Ala Leu Val Val Glu
 20 25 30

Val Leu Glu Glu Asn Tyr His Lys Ala Asp Ile Val Gly Phe Ala Ile
 35 40 45

Ala Asn Glu Asn Gly Asn Phe Phe Ile Pro Thr Asp Thr Ala Leu Ala
 50 55 60

Ser Glu Ala Phe Lys Lys Trp Leu Glu Asp Glu Thr Lys Lys Ser
 65 70 75 80

Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp His Gly Ile
 85 90 95

Glu Leu Lys Gly Val Asp Phe Asp Leu Leu Ile Ala Ser Tyr Leu Leu
 100 105 110

Asn Pro Ser Glu Ser Ser Asp Asp Phe Ala Ser Val Ala Lys Thr Lys
 115 120 125

Gly Tyr Asn Ala Val Gln Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
 130 135 140

Lys Arg Ala Val Pro Asp Glu Glu Lys Leu Ala Glu His Leu Ala Arg
 145 150 155 160

Lys Ala Ala Ala Ile Ser Ala Leu Lys Glu Thr Phe Ile His Glu Leu
 165 170 175

Lys Glu Asn

<210> SEQ_ID NO 124

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 124

Glu Glu Glu Glu Glu Pro Leu Glu Asp Ile Ser Phe Glu Ile Val Glu
 1 5 10 15

Glu Val Thr Glu Glu Met Leu Thr Asp Glu Ser Ala Leu Val Val Glu
 20 25 30

-continued

Val Leu Glu Glu Asn Tyr His Lys Ala Asp Ile Val Gly Phe Ala Ile
35 40 45

Val Asn Glu Asn Gly Asn Phe Phe Ile Pro Thr Asp Thr Ala Leu Ala
50 55 60

Ser Glu Ala Phe Lys Lys Trp Leu Glu Asp Glu Thr Lys Lys Thr
65 70 75 80

Val Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Lys Gly Val Asp Phe Asp Leu Leu Ile Ala Ser Tyr Leu Leu
100 105 110

Asn Pro Ser Glu Thr Asn Asp Asp Phe Ala Ser Val Ala Lys Thr Lys
115 120 125

Gly Tyr Asn Ala Val Gln Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Glu Glu Lys Leu Ala Glu His Leu Ala Arg
145 150 155 160

Lys Ala Ala Ala Ile Ser Ala Leu Lys Glu Thr Phe Ile Gln Glu Leu
165 170 175

Lys Glu Asn

<210> SEQ ID NO 125

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 125

Ala Glu Glu Glu Lys Pro Leu Glu Glu Met Glu Phe Ala Ile Ala Asp
1 5 10 15

Glu Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Lys Ala Trp Leu Ala Asp Glu Thr Lys Lys Ser
65 70 75 80

Met Phe Asp Ala Lys Arg Ala Ile Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Asp Ala Asp Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Arg Ala Leu Glu Arg Pro Phe Leu Asp Glu Leu
165 170 175

Arg Asn Asn

<210> SEQ ID NO 126

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 126

Ala Glu Glu Glu Lys Pro Leu Ala Glu Met Glu Phe Ala Ile Ala Asp
1 5 10 15

Ser Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30

Val Val Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45

Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu Ala
50 55 60

Asp Pro Gln Phe Leu Ala Trp Leu Gly Asp Glu Thr Lys Lys Lys Ser
65 70 75 80

Met Phe Asp Ser Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly Ile
85 90 95

Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
100 105 110

Asn Pro Ala Gln Ala Ala Gly Asp Val Ala Ala Val Ala Lys Met Lys
115 120 125

Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Ala
130 135 140

Lys Arg Ser Val Pro Asp Glu Pro Thr Leu Ala Glu His Leu Val Arg
145 150 155 160

Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Glu Leu
165 170 175

Arg Arg Asn

<210> SEQ ID NO 127

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 127

cagccagccg cagcacgttc gctcatagga gatatggtag agccgc 46

<210> SEQ ID NO 128

<211> LENGTH: 51

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 128

gagagaattt gtaccacctc ccacggggca catagcagtc ctagggacag t 51

<210> SEQ ID NO 129

<211> LENGTH: 22

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 129

ggcttggctc tgctaacacg tt 22

<210> SEQ ID NO 130

<211> LENGTH: 22

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<400> SEQUENCE: 130

ggacgttgt aatgtccgct cc

22

<210> SEQ ID NO 131
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<400> SEQUENCE: 131

ctgcatacga cgtgtct

17

<210> SEQ ID NO 132
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<400> SEQUENCE: 132

accatctatg actgtacgcc

20

<210> SEQ ID NO 133
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<400> SEQUENCE: 133

cgccagggtt ttcccagtca cgac

24

<210> SEQ ID NO 134
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<400> SEQUENCE: 134

agaacgggaa gcttgtcatc

20

<210> SEQ ID NO 135
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<400> SEQUENCE: 135

cgaacatggg ggcattcag

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What is claimed is:

1. A protein comprising an amino acid sequence that has at least 98% sequence identity with at least one sequence selected from the group consisting of SEQ ID NOs: 44, 45, 54, 55, 64, 77, 88, 90, 91, 92 and 106.

2. A protein according to claim 1, further comprising DNA polymerase activity.

60 3. A protein according to claim 1, wherein the protein is capable of replicating DNA.

4. A protein according to claim 3, wherein the protein is capable of replicating DNA in an isothermal amplification reaction.

65 5. A protein according to claim 1 in a storage buffer, or a reaction buffer.

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6. A protein according to claim **5**, wherein the buffer further comprises temperature dependent inhibitor of polymerase activity.

7. A protein according to claim **1**, fused to a peptide either directly or by means of a linker.

8. A protein according to claim **1**, wherein the buffer further comprises dNTPs.

9. A DNA encoding the protein of claim **1**.

10. A host cell comprising the DNA according to claim **9**.

11. A method for determining whether a protein according to claim **1** has improved polymerase activity compared with a wild type Bst polymerase; comprising synthesizing a protein according to claim **1**; and determining the polymerase activity.

12. A method according to claim **11**, wherein characterizing the polymerase activity further comprises: determining in comparison with a wild type Bst polymerase, at least one improved property selected from the group consisting of: thermostability; stability in storage; tolerance to salt; performance in isothermal amplification; strand displacement; kinetics; processivity; fidelity; altered ribonucleotide incorporation; 2'-deoxyuridine 5'-triphosphate incorporation; reverse transcriptase activity; and modified nucleotide incorporation.

13. A method, comprising:

(a) selecting a protein according to claim **1**; and
(b) expressing the protein as a fusion protein with an additional peptide at an end of the amino acid sequence, the additional peptide attached either directly or by means of a linker.

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14. A method of isothermal amplification, comprising:
(a) providing a reaction mixture comprising a protein according to claim **1**, primers and dNTPs;
(b) combining a target DNA with the preparation; and
(c) amplifying the target DNA at a temperature less than 90° C.

15. A method according to claim **14**, wherein the amplification reaction results in a quantitative measure of the amount of target DNA in the preparation.

16. A protein according to claim **1** further characterized by one or more improved properties for isothermal amplification compared with a wild type Bst polymerase, selected from the group consisting of:

- (a) an increased reaction speed where the increase is at least 10% and as much as 200%, 500% or 1000%;
- (b) an increased temperature stability in the range of 50° C.-100° C., 50° C.-90° C. or 60° C. -90° C.;
- (c) an increased salt tolerance in the range of 10 mM-1 M, or 20 mM-200 or 500 mM monovalent salt;
- (d) an increase in storage stability at 25° C., retaining at least 50% activity over 45 weeks, over 1 year or over 2 years;
- (e) an enhanced dUTP tolerance of the range of an increase of 50% to 100% dUTP; and
- (f) an increased reverse transcriptase activity by at least 2 fold.

17. A protein according to claim **16**, having at least two or three or four or five or six of the improved properties.

* * * * *